

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 05:22:44 ; Search time 10357.4 Seconds
(without alignments)
7013.028 Million cell updates/sec

Title: US-09-937-636-1
Perfect score: 1536
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_cm.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1244.8	81.0	3124	9 AF311905	Homo sapi
2	1100.4	71.6	2374	6 CO842614	Sequence
3	1100.4	71.6	2374	9 AK122619	Homo sapi
4	1082	70.4	2565	6 AX365516	Sequence
5	1078.8	70.2	2764	6 CQ767791	Sequence
6	1078.8	70.2	2764	6 AX376050	Sequence
7	1078.8	70.2	2764	9 AY358337	Homo sapi
8	956.2	62.3	2208	6 AX365530	Sequence
9	956.2	62.3	3012	9 AF301007	Homo sapi
10	956.2	62.3	3024	6 AX365542	Sequence
11	954.6	62.1	2176	9 AF310233	Homo sapi
12	869.2	56.6	2321	6 AX497858	Sequence
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Homo sapiens sialic acid-binding Ig-like lectin 10 (SIGLEC10) mRNA, complete cds.
ACCESSION AF311905
VERSION AF311905.1 GI:15217165
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3124)
AUTHORS Li.N., Zhang.W., Wan.T., Zhang.J., Chen.T., Yu.Y., Wang.J. and Cao.X.
TITLE Cloning and characterization of Siglec-10, a novel sialic acid binding member of the Ig superfamily, from human dendritic cells
J. Biol. Chem. 276 (30), 28106-28112 (2001)
MEDLINE 21359381
PubMed 11358961
REFERENCE 2 (bases 1 to 3124)
AUTHORS Li.N., Zhang.W., Wan.T. and Cao.X.
TITLE Direct Submission
Submitted (15-AUG-2001) Department of Immunology, Second Military Medical University, 800 Xiangyin Rd., Shanghai 200433, P.R.China
JOURNAL
FEATURES
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REFERENCE

1. (bases 1 to 2374)

Isogai, T. and Yamamoto, J.

Direct Submission

SOURCE

COMMENT

Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5' & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.

FEATURES

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ORIGIN

Query Match 71.6%; Score 1100.4; DB 9; Length 2374;
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Matches 1288; Conservative 0; Mismatches 6; Indels 174; Gaps 1;

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RESULT 4

AX365516

LOCUS

AX365516 2565 bp DNA linear PAT 15-FEB-2002

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ACCESSION	Q767791	Q767791		
VERSION	Q767791.1	GI:45108134		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			


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LOCUS
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Sequence 27 from Patent WO0208257.
ACCESSION
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VERSION
AX365542.1 GI:18697098
KEYWORDS
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SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
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AUTHORS
Longphre, M., Chang, H. and Whitney, G.
TITLE
Novel siglecs and uses thereof
JOURNAL
Patent: WO 0208257-A 27 31-JAN-2002;
BRISTOL-MYERS SQUIBB COMPANY (US)
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Location/Qualifiers
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LOCUS      Homo sapiens sialic acid binding immunoglobulin-like lectin 10
DEFINITION      (SIGLEC10) mRNA, complete cds.
ACCESSION      AF310233
VERSION      AF310233.1 GI:14164612
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelesostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Munday,J., Kerr,S., Ni,J., Cornish,A.L., Zhang,J.Q., Nicoll,G.,
Floyd,H., Mattei,M.-G., Moore,P., Liu,P. and Crocker,P.R.
Identification, characterization and leucocyte expression of
Siglec-10, a novel human sialic acid-binding receptor
Biochem. J. 355 (Pt 2), 489-497 (2001)
BIOCHEM      J. 355 (Pt 2), 489-497 (2001)
MEDLINE      21181584
PUBMED      11284738
REFERENCE      2 (bases 1 to 2176)
AUTHORS      Cornish,A.L., Ni,J. and Crocker,P.R.
TITLE      Direct Submission
JOURNAL      Submitted (02-OCT-2000) School of Biological Sciences, University
of Dundee, Dow Street, Dundee DD6 8AT, Scotland, United Kingdom
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ORIGIN

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Query Match      62.1%; Score 954.6; DB 9; Length 2176;
Best Local Similarity 73.3%; Pred. No. 5.6e-246;
Matches 1532; Conservative 0; Mismatches 4; Indels 555; Gaps 2;

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QY 61 TTCTGATAGAGTGAGGAGTGAGTGATGTCGCGGGGTCGTCGATCTCTGTGCCC 120
DB 98 TTCTGATAGAGTGAGGAGTGAGTGATGTCGCGGGGTCGTCGATCTCTGTGCCC 157
QY 121 TGCTCTTTCTCTACCCGCGAGGAGTGGACAGGGTCTACCCAGCTTATGGCTACTGG 180
DB 158 TGCTCTTTCTCTACCCGCGAGGAGTGGACAGGGTCTACCCAGCTTATGGCTACTGG 217
QY 181 TTCAAGAGAGTACTGAGACCAACAGAGGTGCTCTGTGGCCACAAACACAGAGTGA 240
DB 218 TTCAAGAGAGTACTGAGACCAACAGAGGTGCTCTGTGGCCACAAACACAGAGTGA 277
QY 241 GAGGTGGAATGAGACCGCGGGCCGATTCACAGTCACTGGGATCCCGCCAGGGGAG 300
DB 278 GAGGTGGAATGAGACCGCGGGCCGATTCACAGTCACTGGGATCCCGCCAGGGGAG 337
QY 301 TGCTCTTTGGTGATGAGACCGCGAGATGCGAGGATGAGTCAAGTCTTCTTGGGGTG 360
DB 338 TGCTCTTTGGTGATGAGACCGCGAGATGCGAGGATGAGTCAAGTCTTCTTGGGGTG 397
QY 361 GAGAGAGGAGTATGAGATATATTTATGACAGATGGGTCTTCTTCTTAAAGTAA 420
DB 398 GAGAGAGGAGTATGAGATATATTTATGACAGATGGGTCTTCTTCTTAAAGTAA 457
QY 421 GCCCTGACTCAGAGGCTGATGTCTACATCCCGAGAGCCCTGAGCGCGGGCAGCGGTG 480
DB 458 GCCCTGACTCAGAGGCTGATGTCTACATCCCGAGAGCCCTGAGCGCGGGCAGCGGTG 517
QY 481 ACGGTATCTGTGTGTTAACTGGGCTTTGAGGAATGTCACCGCTTCTTCTCTGG 540
DB 518 ACGGTATCTGTGTGTTAACTGGGCTTTGAGGAATGTCACCGCTTCTTCTCTGG 577
QY 541 ACGGGGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
DB 578 ACGGGGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 637
QY 601 AGCTTCAGCGCCAGACCCAGGACACGACGACCTCACTGCGATGAGTGTCTCTCC 660
DB 638 AGCTTCAGCGCCAGACCCAGGACACGACGACCTCACTGCGATGAGTGTCTCTCC 697
QY 661 AGAAGGGGTGAGCGCACAGAGGACCGTCCGACTCCGCTGTCGCTATGCTCCCGCAGAGAC 720
DB 698 AGAAGGGGTGAGCGGTACAGAGGACCGTCCGACTCCGCTGTCGCTATGCTCCCGCAGAGAC 757
QY 721 CTTGTTATCAGCATTTACGTGACACACGCGCAG----- 754
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DB 758 CTTGTTATCAGCATTTACGTGACAAACAGCGCCCTGGAGCCCCAGCCCCAGGAAAT 817
QY 755 ----- 754
DB 818 GTCCCATACCTTGAAGCCCAAAAGGCCAGTTCCTTGGGCTCCTCTGTGCTGCTACAGC 877
QY 755 ----- 754
DB 878 CAGCCCCCTGACACACTGAGTGGGTCTGTGAGAACAGAGTCTCTCTCTCTCTCTCTCC 937
QY 755 ----- 754
DB 938 TGGGGCCCTAGACCCCTGGGCTGAGGCTGCGCGGGGTGAAGGCTGGGGATTCAGGGCGC 997
QY 755 ----- 754
DB 998 TACACTGCCGAGCGGAGAACAGAGCTTGGCTCTCCAGCAGCGAGCCCTGCTCTCTGTG 1057
QY 755 ---ATCTCTCAGAGAACCTCAGAGTGTATGTTTCCCAAGCAACAGACAGTCTCTGAA 810
DB 1058 CAGTATCTCTCAGAGAACCTCAGAGTGTATGTTTCCCAAGCAACAGACAGTCTCTGAA 1117
QY 811 AACCTTGGGAAACGCGACGTCTCTCCAGTACTGAGGGGCCAAAGCTTGTCTGTCTGT 870
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DB 1178 GTCAACACAGACGACCCCGCAGCGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGC 1237
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DB 1298 GGAGAGTTACCTGCGACGCTCGGACACCCACTGGGCTCCAGACGCTCTCTCTCAGGCTC 1357
QY 1051 TCCGTGCACT----- 1060
DB 1358 TCCGTGCACTACTCCCGAAGCTCTGGGCCCTCTCTCTCTCTGGAGGCTGAGGCTCTG 1417
QY 1061 ----- 1060
DB 1418 CACTGCAGCTGCTCTCTCCAGCGCCAGCGGCCCTCTCTCTCTCTGTGGCTTGGGAG 1477
QY 1061 ----- 1060
DB 1478 GAGCTGCTGGAGGGGAAACAGACGACGAGTCTCTCTTGGAGTCACTCCCGAGCTCAGCGGG 1537
QY 1061 ----- 1060
DB 1538 CCCTGGGCCAACAGCTCCCTGAGCTCCATGGAGGGCTCAGCTCTGGCCCTCAGGCTCCG 1597
QY 1061 -----ATAAG 1065
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QY 1126 CTTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1185
DB 1718 CTTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1777
QY 1186 ACAGAAACCCCGAGCGCCAGGTTCTCCCGCAGACGAGTCTCTCTCTCTCTCTCTCTCTCTCT 1245
DB 1778 ACAGAAACCCCGAGCGCCAGGTTCTCCCGCAGACGAGTCTCTCTCTCTCTCTCTCTCTCT 1837
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LOCUS	Sialoadhesin family 4 (SAP-4) cDNA.				
DEFINITION	BD011516				
ACCESSION	BD011516				
VERSION	BD011516.1	GI:18639889			
KEYWORDS	JP 2001502359-A/1.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
TITLE	1 (bases 1 to 3099)				
JOURNAL	KIKLY,K.K. and MILLER,C.L.E.				
COMMENT	Sialoadhesin family 4(SAP-4) cDNA				
	Patent: JP 2001502359-A 1 20-FEB-2001;				
	SMITHKLINE BEECHAM CORP				
	OS Homo sapiens (human)				
	PN JP 2001502359-A/1				
	PD 20-FEB-2001				
	PF 27-MAY-1998 JP 1999500864				
	PR 27-MAY-1997 US 60/047572				
	PI KRISTINE KAY KIKLY,CONNIE LYNN ERICKSON MILLER PC				
	A61K38/00,A61K39/395,A61K48/00,C07H21/04,C07K14/435,C07K14/705,PC				
	C07K16/00,				
	PC C07K16/18,C07K16/28,C12N15/01,C12N15/11,C12N15/12,C12N15/63 CC				
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ORIGIN	Query Match 51.2%; Score 787; DB 6; Length 3099;				
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QY	1 ATGCTACTGCCACGTCGTCTGCTCCTCGCTGTGGCGGGTCCAGGCTATGGATGGAGA 60				
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QY	61 TTCTGGATACAGTGCAAGGAGTCAGTGATGGTGGCGAGGCCCTGTGCATCTCTGTGCC 120				
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QY	121 TGTCTTTCTCTCTACCCCGACAGAGCTGGACAGGCTACCCAGGCTTATGGCTACTGG 180				
Db	171 TGTCTTTCTCTACCCCGACAGAGCTGGACAGGCTTATGGCTACTGGCTACTGG 230				
QY	181 TTCAAACGAGTACTGAGACAACCAAGGGTGTCTCTGTGGCCAAACACCACAGAGTCGA 240				
Db	231 TTCAAACGAGTACTGAGACAACCAAGGGTGTCTCTGTGGCCAAACACCACAGAGTCGA 290				
QY	241 GAGGTGGAATGACACCGGGCCGATTTCAGTCTACTGGGATCCGCCAAGGGGAAC 300				
Db	291 GAGGTGGAATGACACCGGGCCGATTTCAGTCTACTGGGATCCGCCAAGGGGAAC 350				
QY	301 TGCTCTTGTGTGATCAGAGACGCCAGATGCAGGATCAGTCACTACTTCTTTCCGGTG 360				
Db	351 TGCTCTTGTGTGATCAGAGACGCCAGATGCAGGATCAGTCACTACTTCTTTCCGGTG 410				
QY	361 GAGAGGAAGCTATGTGAGATAAATTCATGAACGATGGTCTTTCTTAAAGTAACA 420				
Db	411 GAGAGGAAGCTATGTGAGATAAATTCATGAACGATGGTCTTTCTTAAAGTAACA 470				
QY	421 GCCCTGACTCAGAAGCTGTATGTACATCCCCGAGACC----- 459				
Db	471 GTGCTCAGTTCAGCCCAAGCCAGGACCAACACCCACCTCACCTGCCATGTGGAC 530				
QY	460 -----CTGAGCCCGGGCAGCCGGTAGCGGT 485				

817 GACAGCCAGCCCTGCGACATGAGTGGTCTCTGAGAACAGAGTCTCTCTCTCGTCC 876
842 CTGCGATGTGACATCTCTCCAGAAAGGGTGTGAGGCGACAGAGACCGCTCGGACTCCGTGT 701
877 CATCCCTGGGCGCTAGACCCCTGGGCTGGAGTGTCCCGGGTGAAGGTCTGGGATTCG 936
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805 CTGGAACAACTTGGGAACGGCACGTCTCTCCAGTACTGAGGAGGCCAAAGCCTGTGCTTG 864
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1061 ----- 1060
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1240 AATGTGTCCGAGCGGTGCGCCCTCTGGCTAGAAAGCGGAATCAGAAAGCCACCAAAAC 1299
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1837 AGTCTCGGACCCCTCTCTCAGCAGGTGCTCTCCCGCAGATCAAGAGAAAGCCAGAAA 1896
1360 AAGCAGTATCAGTTGCCAGTTTCCCGAGAACCCAAATCATCCACTCAAGCCCCAGAAATCC 1419
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QY 1420 CAGGAGAGCCAGAGAGAGTCTCATTTATGCCACGCTCAAATTTCCAGGCGTCCAGACCCAGG 1479
Db 1957 CAGGAGAGCCAGAGAGAGTCTCATTTATGCCACGCTCAAATTTCCAGGCGTCCAGACCCAGG 2016
QY 1480 CCGTGGAGCCCGGATGCCCAAGGGCACCCAGGCGGATTTATGCAAGTCAAGTTCCAA 1536
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Job time : 10392.4 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 05:07:09 ; Search time 1055.14 Seconds
(without alignments)
7641.758 Million cell updates/sec

Title: US-09-937-636-1
Perfect score: 1536
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: Geneseqn2003cs:.*
11: Geneseqn2003ds:.*
12: Geneseqn2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1536	100.0	1536	3 AAA37847	Aaa37847 Human obe
2	1082	70.4	2565	6 ABK43360	Abk43360 DNA encod
3	1078.8	70.2	2764	2 AAZ34109	Aaz34109 Human PRO
4	1078.8	70.2	2764	3 AAC78510	Aac78510 Human PRO
5	1078.8	70.2	2764	4 AAS45983	Aas45983 Human DNA
6	1078.8	70.2	2764	8 ACA89433	Aca89433 Novel hum
7	1078.8	70.2	2764	8 ACA89433	Aca89433 cDNA enco
8	1078.8	70.2	2764	8 ACA73443	Aca73443 Human sec
9	1078.8	70.2	2764	8 ACA05758	Aca05758 Human sec
10	1078.8	70.2	2764	8 ACA66592	ACA66592 cDNA enco
11	1078.8	70.2	2764	8 ACP20167	Acf20167 Human sec
12	1078.8	70.2	2764	8 ACF19553	Acf19553 Human sec
13	1078.8	70.2	2764	8 ACD21841	Acid21841 Human sec
14	1078.8	70.2	2764	8 ACF13006	Acf13006 Human sec
15	1078.8	70.2	2764	8 ACD25109	Acid25109 Human sec
16	1078.8	70.2	2764	8 ACF00158	Acf00158 Human sec
17	1078.8	70.2	2764	8 ACA72215	ACA72215 Novel hum
18	1078.8	70.2	2764	8 ACD47339	Acid47339 Novel hum
19	1078.8	70.2	2764	8 ACD18200	Acid18200 Human sec
20	1078.8	70.2	2764	8 ACD08207	Acid08207 Human sec
21	1078.8	70.2	2764	8 ACA88641	ACA88641 Novel hum

ALIGNMENTS

RESULT 1
AAA37847
ID AAA37847 standard; DNA; 1536 BP.
XX
AC AAA37847;
DT 12-FEB-2001 (first entry)
XX
DE Human obesity protein binding protein-2 homologue coding sequence #1.
XX
KW Human obesity protein binding protein-2 homologue; hOB-BP2h; obesity;
KW obesity-related disorder; therapy; ds.
XX
OS Homo sapiens.
XX
FH Key
CDS Location/Qualifiers
FT 1..1536
FT /*tag= a
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XX
PN WC200059942-A2.
XX
PD 12-OCT-2000.
XX
PF 22-MAR-2000; 2000WO-US006682.
XX
PR 02-APR-1999; 99US-0127667P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Su EW, Wei J;
XX
DR WPI: 2000-664992/64.
XX
P-PSDB; AAY97542.
XX
PT New human obesity protein binding protein-2 homologue nucleic acids,
PT polynucleotides and polypeptides useful for producing medicament for
PT treating obesity and/or obesity-related disorders.
XX
PS Claim 3; Page 85; 92pp; English.
XX
CC This sequence encodes a human obesity protein binding protein-2 homologue
CC (hOB-BP2h) of the invention. The hOB-BP2h nucleic acids and polypeptides
CC may be used for the manufacture of a medicament for the treatment of

22 1078.8 70.2 2764 8 ACA70083 Human sec
23 1078.8 70.2 2764 8 ACD12305 Novel hum
24 1078.8 70.2 2764 8 ACC74220 Human sec
25 1078.8 70.2 2764 8 ACD15848 Human sec
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33 1078.8 70.2 2764 8 ACD13962 Human PRO
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35 1078.8 70.2 2764 8 ACC88487 Human sec
36 1078.8 70.2 2764 8 ACD21227 Human sec
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38 1078.8 70.2 2764 8 ABX92481 cDNA enco
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PA	(BRIM) BRISTOL-MYERS SQUIBB CO.	QY	460	-----CTGAGCCCGGCGAGCCGGTACCGGT	485
XX		Db	609	TTCTCCAGAAAGGGTGTGAGGCGCAGAGGACCGTCCGACTCCGTGTGGCTTATGCCCCC	668
XX	Longphre M, Chang H, Whitney G;	QY	486	CATCTGTGTGTTTAACTGGGCTTTGAGGAATGTCCACCCCTTCTTTCTCTGAGCGG	545
XX	WPI; 2002-241565/29.	Db	669	AGAGACCTTGTGTATCAGCATTTACGTGACAAACGCCAGCCCTGGAGCCCGAGCCCGAC	728
XX	P-PSDB; AAU87074.	QY	546	GGCTCCCTCTCTCTCCCAAGGAAACCAACACGACCTCCACATTTCTCAGTGTCTCAGTT	605
PT	Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein	Db	729	GGAAATGTCCCATACCTCGAAGCCCAAAAGGCCAGTTCTCTGGGCTCTCTGTGCTGCT	788
PT	moieties useful for treating immune system diseases such as asthma,	QY	606	CACGCCCGAGACCCAGGACCCAC-----GACACCGACCTCAC	641
PT	leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.	Db	789	GACGCCAGCCCGCTGCGCACACTGAGCTGGGTCTGTGAGAACAGAGTCTCTCTCTGCTCC	848
PS	Claim 11; Fig 2A; 209pp; English.	QY	642	CTGCCATGTGACCTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGT	701
XX		Db	849	CATCCTCTGGGCGCTAGACCCCTGGGGCTGGAGCTGCCGGGTGAAGGCTGGGGATCA	908
CC	The invention relates to an isolated SIGLEC (sialic acid-binding Ig-	QY	702	GGCTATGCCCCCAGAGACCTTGTATCAGCATTTTACGTGACAAACAGCGC-----	752
CC	related lectin) protein (I). Pharmaceutical compositions comprising (I)	Db	909	GGCGCTACCTGTCGCGAGCGAGAACAGGCTTGGCTCCGACGACGAGCCCTGGACCTC	968
CC	are useful for treating immune system diseases such as asthma, leukaemia	QY	753	-----AGATCTCTCCAGAGAACCTGAGAGTGATGTTTCCCAAGCAAAACAGGACAGTC	804
CC	or other allergic or inflammatory diseases. Extracellular domains of (I)	Db	969	TCGTGCGAGTATCTCTCAGAGAACCTGAGAGTGATGTTTCCCAAGCAAAACAGGACAGTC	1028
CC	represent potential markers for screening, diagnosis, prognosis, follow-	QY	805	CTGGAAAACTTGGGAAACGGACGCTCTCTCCAGTACTTGGAGGGCCAAAGCTGTGCTG	864
CC	up assays, and imaging methods. (I) is useful as a target for drugs which	Db	1029	CTGGAAAACTTGGGAAACGGACGCTCTCTCCAGTACTTGGAGGGCCAAAGCTGTGCTG	1088
CC	inhibit inflammation, tissue damage and remodeling in asthma, and	QY	865	GTCTGTGTACACACAGCAGACCCCGCCAGCCAGGCTGAGCTTGACCCACAGGGGACAGTT	924
CC	inflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's	Db	1089	GTCTGTGTACACACAGCAGACCCCGCCAGCCAGGCTGAGCTTGACCCACAGGGGACAGTT	1148
CC	disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is	QY	925	CTGAGCCCTCTCCAGCCCTCAGACCCCGGGTCTCTGGAGCTGCTCTGGGTTCAAGTGAG	984
CC	also useful for monitoring the course of disease or disorders, and for	Db	1149	CTGAGCCCTCTCCAGCCCTCAGACCCCGGGTCTCTGGAGCTGCTCTGGGTTCAAGTGAG	1208
CC	identifying agents that bind with and/or modulate the biological activity	QY	985	CACGAGAGAGATTACCTGCGACCGCTCGGACCCACTGGGCTCCGACGAGCTCTCTCTC	1044
CC	of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are	Db	1209	CACGAGAGAGATTACCTGCGACCGCTCGGACCCACTGGGCTCCGACGAGCTCTCTCTC	1268
CC	useful in diagnosis and/or prognosis methods, and to detect the presence	QY	1045	AGCCTCTCGTGCATCTAAGAGGGACTCATCTCAACGGCATTTCTCAATGGAGCGTTT	1104
CC	and/or amount of SIGLEC-BMS nucleotide sequences and/or SIGLEC-BMS	Db	1269	AGCCTCTCGTGCATCTAAGAGGGACTCATCTCAACGGCATTTCTCAACGGAGCGTTT	1328
CC	proteins in a biological sample. (II) are useful as nucleic acid probes	QY	1105	CTGGGAATCGGCATCAACGGCTCTCTTTTCTCTGCTGGCCCTGATCATCATGAAGATT	1164
CC	are useful for screening genomic library to isolate a genomic clone of	Db	1329	CTGGGAATCGGCATCAACGGCTCTCTTTTCTCTGCTGGCCCTGATCATCATGAAGATT	1388
CC	SIGLEC gene. SIGLEC-BMS gene copy number is determined for detecting	QY	1165	CTACCGAAGAGACGAGCTCAGACAGAAACCCCGAGGCCAGGTTCTCCCGGCACAGCAGC	1224
CC	diseases or disorders associated with SIGLEC-BMS transcripts or proteins.	Db	1389	CTACCGAAGAGACGAGCTCAGACAGAAACCCCGAGGCCAGGTTCTCCCGGCACAGCAGC	1448
CC	The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells	QY	1225	ATCTCGAATTACATCAATGTGTCCTCGAGCGCTGGCCCTCGGCTCAGAGCGGAATCAG	1284
CC	expressing SIGLEC-BMS proteins and in diagnostic imaging technology.	Db	1449	ATCTCGAATTACATCAATGTGTCCTCGAGCGCTGGCCCTCGGCTCAGAGCGGAATCAG	1508
CC	ABK43360-ABK43411 represent human SIGLEC coding sequences and PCR primers	QY	1285	AAAGCCACACAAACAGTCTCGGACCCCTCTTCCACAGGTCCTCCCTCCCGCAATCA	1344
CC	of the invention	Db	1509	AAAGCCACACAAACAGTCTCGGACCCCTCTTCCACAGGTCCTCCCTCCCGCAATCA	1568
XX	Sequence 2565 BP; 627 A; 765 C; 656 G; 517 T; 0 U; 0 Other;	QY	1345	AAGAAAGAACCAAGAAAAGCAGTATCAGTTGCCAGGTTTCCAGAAACCCCAATCATCCACT	1404
XX	Query Match 70.4%; Score 1082; DB 6; Length 2565;	Db	1569	AAGAAAGAACCAAGAAAAGCAGTATCAGTTGCCAGGTTTCCAGAAACCCCAATCATCCACT	1628
XX	Best Local Similarity 81.6%; Pred. No. 1.2e-291;	QY	1405	CAAGCCCGAGAAATCCCGAGAGCCACAGAGCTCCGATTTATGACACGCTCAACTCCCA	1464
XX	Matches 1331; Conservative 0; Mismatches 205; Indels 96; Gaps 3;	Db	1629	CAAGCCCGAGAAATCCCGAGAGCCACAGAGAGTCCATTATGACACGCTCAACTCCCA	1688
QY	1 ATGCTACTGCGACCTGCTGCTCTCTGCTGCTGGGGTCCAGGCTATGGATGGGAGA	QY	1	ATGCTACTGCGACCTGCTGCTCTCTGCTGCTGGGGTCCAGGCTATGGATGGGAGA	60
Db	129 ATGCTACTGCGACCTGCTGCTCTCTGCTGCTGGGGTCCAGGCTATGGATGGGAGA	Db	129	ATGCTACTGCGACCTGCTGCTCTCTGCTGCTGGGGTCCAGGCTATGGATGGGAGA	188
QY	61 TTCTGGATACAGTGACAGGAGTCACTGCTGCTGGGGTCTGCTGCTGCTGCTG	QY	61	TTCTGGATACAGTGACAGGAGTCACTGCTGCTGGGGTCTGCTGCTGCTGCTG	120
Db	189 TTCTGGATACAGTGACAGGAGTCACTGCTGCTGGGGTCTGCTGCTGCTGCTG	Db	189	TTCTGGATACAGTGACAGGAGTCACTGCTGCTGGGGTCTGCTGCTGCTGCTG	248
QY	121 TGCTCTTTCTTCTACCCCGACAGGACTGACAGGGTCTACCCAGCTTATGGCTACTG	QY	121	TGCTCTTTCTTCTACCCCGACAGGACTGACAGGGTCTACCCAGCTTATGGCTACTG	180
Db	249 TGCTCTTTCTTCTACCCCGACAGGACTGACAGGGTCTACCCAGCTTATGGCTACTG	Db	249	TGCTCTTTCTTCTACCCCGACAGGACTGACAGGGTCTACCCAGCTTATGGCTACTG	308
QY	181 TTCAAGCAGTACTGAGACCAACAGGGTCTCTGCTGCTGCTGCTGCTGCTGCTG	QY	181	TTCAAGCAGTACTGAGACCAACAGGGTCTCTGCTGCTGCTGCTGCTGCTGCTG	240
Db	309 TTCAAGCAGTACTGAGACCAACAGGGTCTCTGCTGCTGCTGCTGCTGCTGCTG	Db	309	TTCAAGCAGTACTGAGACCAACAGGGTCTCTGCTGCTGCTGCTGCTGCTGCTG	368
QY	241 GAGGTGAAATGACACCCCGGGCCGATTCAGCTCACTGGGATCCCGCCAAAGGGGAA	QY	241	GAGGTGAAATGACACCCCGGGCCGATTCAGCTCACTGGGATCCCGCCAAAGGGGAA	300
Db	369 GAGGTGAAATGACACCCCGGGCCGATTCAGCTCACTGGGATCCCGCCAAAGGGGAA	Db	369	GAGGTGAAATGACACCCCGGGCCGATTCAGCTCACTGGGATCCCGCCAAAGGGGAA	428
QY	301 TGCTCTTTGATCAGACCGCGCAGATCAGAGTCACTGCTGCTGCTGCTGCTGCTG	QY	301	TGCTCTTTGATCAGACCGCGCAGATCAGAGTCACTGCTGCTGCTGCTGCTGCTG	360
Db	429 TGCTCTTTGATCAGACCGCGCAGATCAGAGTCACTGCTGCTGCTGCTGCTGCTG	Db	429	TGCTCTTTGATCAGACCGCGCAGATCAGAGTCACTGCTGCTGCTGCTGCTGCTG	488
QY	361 GAGAGAGAAAGCTATGTGAGATATAATTTCAATGAAAGTGGTCTTTTCTAAAGTA	QY	361	GAGAGAGAAAGCTATGTGAGATATAATTTCAATGAAAGTGGTCTTTTCTAAAGTA	420
Db	489 GAGAGAGAAAGCTATGTGAGATATAATTTCAATGAAAGTGGTCTTTTCTAAAGTA	Db	489	GAGAGAGAAAGCTATGTGAGATATAATTTCAATGAAAGTGGTCTTTTCTAAAGTA	548
QY	421 GCCTTGACTCAGAGCCTGATGCTACATCCCGAGAC-----	QY	421	GCCTTGACTCAGAGCCTGATGCTACATCCCGAGAC-----	459
Db	549 GTGCTAGCTTACGCCCGACCCCGAGGACCAACACCGACCTCACCTGCCATGTGGAC	Db	549	GTGCTAGCTTACGCCCGACCCCGAGGACCAACACCGACCTCACCTGCCATGTGGAC	608

1465 GGCCTCAGACCCAGCCCTGAGCCCGGATGCTCCAGGCGCACCCAGCGGATTATGCAGAA 1524
1689 GGCCTCAGACCCAGCCCTGAGCCCGGATGCTCCAGGCGCACCCAGCGGATTATGCAGAA 1748
1525 GTCAAGTTCCAA 1536
1749 GTCAAGTTCCAA 1760

RESULT 3
AAZ34109
TO AAZ34109 standard; cDNA; 2764 BP.
AAZ34109;
07-DEC-1999 (first entry)
DE Human PRO940 nucleotide sequence.
Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
probe; blood coagulation disorder; cancer; cellular adhesion disorder;
secreted protein; transmembrane protein; ss.

OS Homo sapiens.
EN WO9946281-A2.
XX 16-SEP-1999.
XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077632P.
XX 11-MAR-1998; 98US-0077641P.
XX 11-MAR-1998; 98US-0077649P.
XX 12-MAR-1998; 98US-0077791P.
XX 13-MAR-1998; 98US-0078004P.
XX 17-MAR-1998; 98US-00040220.
XX 20-MAR-1998; 98US-0078886P.
XX 20-MAR-1998; 98US-0078910P.
XX 20-MAR-1998; 98US-0078916P.
XX 20-MAR-1998; 98US-0078939P.
XX 25-MAR-1998; 98US-0079294P.
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XX 27-MAR-1998; 98US-0079664P.
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XX 30-MAR-1998; 98US-0079920P.
XX 30-MAR-1998; 98US-0079923P.
XX 31-MAR-1998; 98US-0080105P.
XX 31-MAR-1998; 98US-0080107P.
XX 31-MAR-1998; 98US-0080165P.
XX 31-MAR-1998; 98US-0080194P.
XX 01-APR-1998; 98US-0080327P.
XX 01-APR-1998; 98US-0080328P.
XX 01-APR-1998; 98US-0080333P.
XX 01-APR-1998; 98US-0080334P.
XX 08-APR-1998; 98US-0081049P.
XX 08-APR-1998; 98US-0081070P.
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XX 09-APR-1998; 98US-0081105P.
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XX 15-APR-1998; 98US-0081817P.
XX 15-APR-1998; 98US-0081838P.
XX 15-APR-1998; 98US-0081952P.
XX 15-APR-1998; 98US-0081955P.
XX 21-APR-1998; 98US-0082568P.
XX 21-APR-1998; 98US-0082569P.
XX 22-APR-1998; 98US-0082700P.
XX 22-APR-1998; 98US-0082704P.

22-APR-1998; 98US-0082804P.
23-APR-1998; 98US-0082767P.
23-APR-1998; 98US-0082796P.
27-APR-1998; 98US-0083336P.
28-APR-1998; 98US-0083322P.
28-APR-1998; 98US-0083322P.
29-APR-1998; 98US-0083495P.
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29-APR-1998; 98US-0083495P.
29-APR-1998; 98US-0083500P.
29-APR-1998; 98US-0083545P.
29-APR-1998; 98US-0083554P.
29-APR-1998; 98US-0083559P.
29-APR-1998; 98US-0083559P.
30-APR-1998; 98US-0083742P.
05-MAY-1998; 98US-0084366P.
06-MAY-1998; 98US-0084414P.
06-MAY-1998; 98US-0084414P.
07-MAY-1998; 98US-0084598P.
07-MAY-1998; 98US-0084600P.
07-MAY-1998; 98US-0084627P.
07-MAY-1998; 98US-0084637P.
07-MAY-1998; 98US-0084637P.
07-MAY-1998; 98US-0084637P.
07-MAY-1998; 98US-0084640P.
07-MAY-1998; 98US-0084643P.
13-MAY-1998; 98US-0085323P.
13-MAY-1998; 98US-0085338P.
13-MAY-1998; 98US-0085339P.
15-MAY-1998; 98US-0085571P.
15-MAY-1998; 98US-0085577P.
15-MAY-1998; 98US-0085580P.
15-MAY-1998; 98US-0085582P.
15-MAY-1998; 98US-0085689P.
15-MAY-1998; 98US-0085697P.
15-MAY-1998; 98US-0085700P.
15-MAY-1998; 98US-0085704P.
18-MAY-1998; 98US-0086023P.
22-MAY-1998; 98US-0086392P.
22-MAY-1998; 98US-0086414P.
22-MAY-1998; 98US-0086414P.
22-MAY-1998; 98US-0086430P.
22-MAY-1998; 98US-0086486P.
28-MAY-1998; 98US-0087098P.
28-MAY-1998; 98US-0087106P.
28-MAY-1998; 98US-0087208P.
30-JUL-1998; 98US-0094651P.
11-SEP-1998; 98US-0100038P.

(GETH) GENENTECH INC.

Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

WPI; 1999-551358/46.
P-PSDB; AAY41724.

New secreted and transmembrane polypeptides and their polynucleotides,
useful for treating blood coagulation disorders, cancers and cellular
adhesion disorders.

Claim 2; Fig 92; 530pp; English.

The present invention describes secreted and transmembrane polypeptides
and their polynucleotides. The nucleotide sequences are useful as sources
of probes, primers, for chromosome mapping, and for generation of
antisense sequences. They can also be used to create transgenic animals.
The proteins can be used to treat a variety of diseases and disorders,
depending on their function. Diseases that may be treated include blood
coagulation disorders, cancers and cellular adhesion disorders. They may
also be used to raise antibodies. AAZ33891 to AAZ4338, and AAY41685 to
AAZ41774 represent polynucleotide and polypeptide sequence given in the
exemplification of the present invention

Sequence 2764 BP; 689 A; 798 C; 717 G; 560 T; 0 U; 0 Other;

460	CTGGAGCCCGGCGACGCGTGA	485
526	TTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTTGCGCTATGCCCC	585
486	CATCTGTGTGTTTAACTGGGCGTTTCAGGAAATGTCACCCCTTCTTTTCTCCTGGAACGG	545
586	AGAGACTTGTATCAGCATTTCACTGTGACACACGCGAGCCCTGGAGCCCGAGCCCAAG	645
546	GGCTGCCCTCTCTCCCAAGGAACCAACCGAAGTCCCACTTCTCTCAGTGTCTCAGTT	605
646	GGAAATGTCCCAATACCTGGAAGGCCAAAAGGCGAGTCTCTGCGGTCTCTGTGTGCTGT	705
606	CAGCCCGAGACCCAGGACCA	661
706	GACAGCGAGCCCTCCCACTGAGCTGGGTCTTCGAGAACAGATCTCTCTCTGCTC	765
642	CTCCCATGTGGACTTCTCCAGAAAGGTGTGAGCGCACAGAGACCGTCCGATCCGTT	701
766	CATCCCTGGGCGCTAGACCCCTGGGCTGGAGCTGCCGGGTGAAGCTGGGGATCA	825
702	GGCCTATGCCCCCAGAGACTTGTATTACAGATTTTCACTGACAAACAGCC	752
826	GGCGGCTACACTTGGCGAGCGGAGAACAGCTTGGTCCGACGAGGAGCCCTGGACCTC	885
753	AGATCCTCCAGAGAACTTGAGAGTGAATGGTTTCCCAAGCAAAACAGGACAGT	804
886	TCGTGCGATATCTTCAGAGAACTTGAGATGATGGTTTCCCAAGCAAAACAGGACAGT	945
805	CTGAAACCTTCGGAAACGCGACGTCTCTCCAGTACTTGGAGGGCCAAAGCTGTGCTG	864
946	CTGAAACCTTCGGAAACGCGACGTCTCTCCAGTACTTGGAGGGCCAAAGCTGTGCTG	1005
865	GTCTGTGTACACACAGCAGCCCCCAGCAGAGCTGAGCTGGACCCAGAGGGGACAGGTT	924
1006	GTCTGTGTACACACAGCAGCCCCCAGCAGAGCTGAGCTGGACCCAGAGGGGACAGGTT	1065
925	CTGAGCCCTCCAGAGCCTCAGACCCCGGGTCTCTGGAGCTGCTCGGTTCAAGTGGAG	984
1066	CTGAGCCCTCCAGAGCCTCAGACCCCGGGTCTCTGGAGCTGCTCGGTTCAAGTGGAG	1125
985	CAGAGAGAGATTCACCTGCGAGGTGCGACCGCACTGGGCTCCAGACAGCTCTCTC	1044
1126	CACGAAGAGAGTTCACTCGCAGCTCGGACCCCACTGGGCTCCAGACAGCTCTCTC	1185
1045	AGCTCTCCGTCACATATAAGAGGAGTCACTCTCAACGGCATTTCCAAATGGAGCGTTT	1104
1186	AGCTCTCCGTCACATATAAGAGGAGTCACTCTCAACGGCATTTCCAAACGAGCGTTT	1245
1105	CTGGGAATCGGATCAGGCTCTTTTCTCTGCTGCGCTGTGATCATCATGAAGATT	1164
1246	CTGGGAATCGGATCAGGCTCTTTTCTCTGCTGCGCTGTGATCATCATGAAGATT	1305
1165	CTACGAAGAGAGCGACTCAGACAGAAACCCGAGGCCAGGTTCTCCGGGACAGCAGC	1224
1306	CTACGAAGAGAGCGACTCAGACAGAAACCCGAGGCCAGGTTCTCCGGGACAGCAGC	1365
1225	ATCCTGGATTACATCAATGTGGTCCGACGGCTGGCCCTCTGGCTCAGAAAGCGGAATCAG	1284
1366	ATCCTGGATTACATCAATGTGGTCCGACGGCTGGCCCTCTGGCTCAGAAAGCGGAATCAG	1425
1285	AAGCCACACCAACAGTCTCGGACCCCTCTTCCACAGGTGCTCCCTCCCGAGATCA	1344
1426	AAGCCACACCAACAGTCTCGGACCCCTCTTCCACAGGTGCTCCCTCCCGAGATCA	1485
1345	AAGAAGAACCCAGAAAAAGCAGTATCAGTTGCCAGATTTCACAGAACCAATCATCACT	1404
1486	AAGAAGAACCCAGAAAAAGCAGTATCAGTTGCCAGATTTCACAGAACCAATCATCACT	1545
1405	CAAGCCCCAGAAATCCAGGAGAGCCAGAGAGTCCATTATGCCAGCTCAACTCCCCA	1464
1546	CAAGCCCCAGAAATCCAGGAGAGCCAGAGAGTCCATTATGCCAGCTCAACTCCCCA	1505
1465	GGCGTCAGACCCAGGCTGAGGCCCGGAATGCCAAGGGGACCCAGGCGGATTATGCAGAA	1524

886 TCTGTGAGTATCTCCAGAGAACCTGAGAGTGATGTTTCCCAAGCAAAACAGACAGTC 945
805 CTGGAAACCTTGGGACGCGAGTCTCTCCAGTACTGGAGGGCCAAAGACCTGTGCTCG 864
946 CTGGAAACCTTGGGACGCGAGTCTCTCCAGTACTGGAGGGCCAAAGACCTGTGCTCG 1005
865 GTCTGTGTACACACAGCAGCCCCCAGCCAGCGCTGAGCTGGACCCAGAGGGGACAGGTT 924
1006 GTCTGTGTACACACAGCAGCCCCCAGCCAGCGCTGAGCTGGACCCAGAGGGGACAGGTT 1065
925 CTGAGCCCTTCCAGCCCTCAGACCCCGGGTCTCTGGAGTCTCTGGAGTCTCAAGTGGAG 984
1066 CTGAGCCCTTCCAGCCCTCAGACCCCGGGTCTCTGGAGTCTCTGGAGTCTCAAGTGGAG 1125
985 CACGAAGAGAGTTCACCTGCGACGCTCGGACCCCTGCGGCTCCAGCAGCTCTCTCTC 1044
1126 CACGAAGAGAGTTCACCTGCGACGCTCGGACCCCTGCGGCTCCAGCAGCTCTCTCTC 1185
1045 AGCTCTCTCGTGCATATAGAGGAGTCTCATCTCAAGGCTCTCTCAATGGAGGTTT 1104
1186 AGCTCTCTCGTGCATATAGAGGAGTCTCATCTCAAGGCTCTCTCAATGGAGGTTT 1245
1105 CTGGGATCGGATCAGGCT 1164
1246 CTGGGATCGGATCAGGCT 1305
1165 CTACCGAAGAGCGGACTCAGACAGAAACCCGAGGCGCCAGGTTCTCCCGGACAGCAG 1224
1306 CTACCGAAGAGCGGACTCAGACAGAAACCCGAGGCGCCAGGTTCTCCCGGACAGCAG 1365
1225 ATCTGTGATTTACATCAATGTTGTTCCGACGCTGCGGCTGCGGCTGCGGATCATCA 1284
1366 ATCTGTGATTTACATCAATGTTGTTCCGACGCTGCGGCTGCGGCTGCGGATCATCA 1425
1285 AAAGCCACACCAACAGTCTCTCGGACCCCTCTTCCACAGGTTCTCTCCCGGACAGTCA 1344
1426 AAAGCCACACCAACAGTCTCTCGGACCCCTCTTCCACAGGTTCTCTCCCGGACAGTCA 1485
1345 AAGAAACACGAGAAAGAGTATGATGTCGACGCTGCGGCTGCGGCTGCGGATCATCA 1404
1486 AAGAAACACGAGAAAGAGTATGATGTCGACGCTGCGGCTGCGGCTGCGGATCATCA 1545
1405 CAAGCCACAGAAATCCAGGAGGCAAGAGAGTCTCAATATGCGGCTCAACTTCCCA 1464
1546 CAAGCCACAGAAATCCAGGAGGCAAGAGAGTCTCAATATGCGGCTCAACTTCCCA 1605
1465 GGCCTCAGACCCAGGCTGAGGCGCGGATGCGGAGGCGGATGCGGATGCGGATGCGA 1524
1606 GGCCTCAGACCCAGGCTGAGGCGCGGATGCGGAGGCGGATGCGGATGCGGATGCGA 1665
1525 GTCAGGTTCCAA 1536
1666 GTCAGGTTCCAA 1677

RESULT 7
AC89433
AC89433 standard; cDNA; 2764 BP.
AC89433;
AC89433;
09-JUL-2003 (first entry)
cDNA encoding human PRO polypeptide #59.
Human; PRO polypeptide; secreted protein; transmembrane protein;
chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast;
prostate; rectal; cervical; liver; cancer; TNF-alpha;
tumour necrosis factor-alpha; proliferation; differentiation;
chondrocyte cell; bone disorder; cartilage disorder; sports injury;
arthritis; cytostatic; antiarthritic; osteopathic; gene therapy; gene;
ss.

OS Homo sapiens.
XX US2003036141-A1.
PN 20-FEB-2003.
PD 01-JUL-2002; 2002US-00187597.
XX 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
XX 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
XX 24-OCT-1997; 97US-0063130P.
PR 24-OCT-1997; 97US-0083121P.
XX 28-OCT-1997; 97US-0083540P.
PR 28-OCT-1997; 97US-0063541P.
XX 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
XX 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063870P.
XX 31-OCT-1997; 97US-0064103P.
PR 31-OCT-1997; 97US-0065311P.
XX 13-NOV-1997; 97US-0065612P.
PR 21-NOV-1997; 97US-0066466P.
XX 24-NOV-1997; 97US-0066772P.
PR 24-NOV-1997; 97US-0069335P.
XX 11-DEC-1997; 97US-0069435P.
PR 12-DEC-1997; 97US-0069870P.
XX 17-DEC-1997; 97US-0068017P.
PR 18-DEC-1997; 98US-0077450P.
XX 10-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
XX 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078939P.
XX 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
XX 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
XX 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
XX 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
XX 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
XX 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
XX 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
XX 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
XX 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083559P.
XX 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
XX 07-MAY-1998; 98US-0084633P.
PR 07-MAY-1998; 98US-0084640P.
XX 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
XX 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
XX 18-MAY-1998; 98US-0086023P.
PR 18-MAY-1998; 98US-0086392P.
XX 22-MAY-1998; 98US-0086486P.
PR 22-MAY-1998; 98US-0087098P.
XX 26-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087609P.
XX 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
XX 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
XX 04-JUN-1998; 98US-0088029P.

466 GTGCTCAGCTTACGCGCCAGACCCAGGACCAACACACCGACCTCACCTGCGCATGTGGAC 525
 460 -----CTGGAGCCGGGACGCGGTGACGGT 485
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 486 CATCTGTGTGTTAACTGGGCTTTGAGGAATGTCCACCCCTTTCTTCTCTGGAGGG 545
 586 AGAGACCTTGTATCAGCATTTCACTGACAAACACGCGACCTGTGAGCCCGACGCCAG 645
 546 GGCTGCGCTCTCTCCCAAGGACCAACCAACGACTCCACTTCTCAGTGTCTCAGTT 605
 646 GGAAATGTCATACCTCTGGAGCCCAAAAGGCGAGTTCTGCGGTCTCTGTGTCTGT 705
 606 CACGCCCGACCCAGGACCCAC-----GACACCGACCTCAC 641
 706 GACAGCCAGCCCTGCGCACACTGAGCTGGTCTCTGAGAACAGAGTCTCTCTCGTCC 765
 642 CTGCGATGTGACTTCTCCAGAAAGGTGTAGGCGCACAGAGACCGTCCGACTCCGTGT 701
 766 CATCTCTGGGCGCTAGACCCCTGGGCTGGAGTCCCGGGGTGAGGTGGGGATTCA 825
 702 GGCTATGCGCCCGACAGACCTTGTATCAGCATTTTCACTGTGACAAACGCGC----- 752
 826 GGGCGCTACACTGCGGAGGAGAACAGGCTTGGCTCCCGAGCGAGCCCTGGACCTC 885
 753 -----AGATCTCCAGAGAACCTGAGAGTATGTTTCCCAAGCAACAGACAGATC 804
 886 TCTGTGAGTATCTCCAGAGAACCTGAGAGTATGTTTCCCAAGCAACAGACAGATC 945
 805 CTGGAACCTTGGAGCGGACGCTCTCCAGTACTGAGGCGCAAAAGCTGTGCGCTG 864
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 865 GTCTGTGTACACAGACAGCCCGCCAGCCAGGCTGAGTGTGACCCAGAGGGGACAGTT 924
 1006 GTCTGTGTACACAGACAGCCCGCCAGCCAGGCTGAGTGTGACCCAGAGGGGACAGTT 1065
 925 CTGAGCCCTCCAGCCCTCAGACCCCGGGTCTCTGAGTGTCTCGGTTCAAGTGGAG 984
 1066 CTGAGCCCTCCAGCCCTCAGACCCCGGGTCTCTGAGTGTCTCGGTTCAAGTGGAG 1125
 985 CACGAAGAGAGTTCACTGCGACCGCTCGGACCCACTGGGCTCCAGCAGCTCTCTCT 1044
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 1246 CTGGAAATCGCATCACGGCTCTTTCTCTCTGCTGCGCTGATCATCATGAAGATT 1305
 1165 CTACGAAGAGAGGACTTACAGAGAAACCCCGAGGCGCCAGTTCTCCCGGACAGCAAG 1224
 1306 CTACGAAGAGAGGACTTACAGAGAAACCCCGAGGCGCCAGTTCTCCCGGACAGCAAG 1365
 1225 ATCTGTGATTAATCAATGTGTCTCCGACGCTGCGGCTGCTGAGAGCGGAATCAG 1284
 1366 ATCTGTGATTAATCAATGTGTCTCCGACGCTGCGGCTGCTGAGAGCGGAATCAG 1425
 1285 AAAGCCACACCAACAGTCTTGGACCCCTTTTCCACAGAGTGTCTCTCCCGAGATCA 1344
 1426 AAAGCCACACCAACAGTCTTGGACCCCTTTTCCACAGAGTGTCTCTCCCGAGATCA 1485
 1345 AAGAGAGACCGAGAAAGCGATATCAGTTGCGGCTGCTGAGTTCACGAACCCAAATATCACT 1404
 1486 AAGAGAGACCGAGAAAGCGATATCAGTTGCGGCTGCTGAGTTCACGAACCCAAATATCACT 1545
 1405 CAAGCCCGAGATCCAGGAGAGCAAGAGAGTCTCCATTATGCCAGCTCAACTTCCCA 1464
 1546 CAAGCCCGAGATCCAGGAGAGCAAGAGAGTCTCCATTATGCCAGCTCAACTTCCCA 1605

QY 1465 GGCTCAGACCCAGGCTGTAGGCGCGGATCCCAAGGGACCCAGGCGGATTATGCAGAA 1524
 Db 1606 GGCTCAGACCCAGGCTGTAGGCGCGGATCCCAAGGGACCCAGGCGGATTATGCAGAA 1665
 QY 1525 GTCAAGTTCCAA 1536
 Db 1666 GTCAAGTTCCAA 1677
 RESULT 8
 ID ACA73443 standard; cDNA; 2764 BP.
 XX ACA73443;
 AC ACA73443;
 DT 01-JUL-2003 (first entry)
 XX Human secreted/transmembrane protein (PRO) cDNA #59.
 DE Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
 KW proliferation; differentiation; chondrocyte cells;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.
 XX Homo sapiens.
 XX US2003036146-A1.
 XX 20-FEB-2003.
 XX 02-JUL-2002; 2002US-00187603.
 XX 26-JUN-1998; 98US-00105413.
 PR 16-SEP-1998; 98WO-US019330.
 PR 07-OCT-1998; 98US-00168978.
 PR 07-OCT-1998; 98WO-US021141.
 PR 06-NOV-1998; 98US-00187368.
 PR 01-DEC-1998; 98WO-US025108.
 PR 07-DEC-1998; 98US-00202054.
 PR 03-MAR-1999; 99US-00254311.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380139.
 PR 25-AUG-1999; 99US-00380142.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 18-OCT-1999; 99US-00403297.
 PR 12-NOV-1999; 99US-00423844.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028551.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.

08-NOV-2000; 2000US-00792338.
08-NOV-2000; 2000WO-US030952.
01-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000US-0074259.
20-DEC-2000; 2000WO-US034956.
28-FEB-2001; 2001WO-US006520.
22-MAR-2001; 2001US-00816774.
10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854280.
25-MAY-2001; 2001US-00866028.
01-JUN-2001; 2001WO-US017800.
05-JUN-2001; 2001US-00874503.
20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
18-JUL-2001; 2001US-00908827.
30-JUL-2001; 2001US-00918585.
06-AUG-2001; 2001US-00924419.
13-AUG-2001; 2001US-00929404.
16-AUG-2001; 2001US-00931836.
28-AUG-2001; 2001US-00941992.
29-AUG-2001; 2001WO-US027099.
04-SEP-2001; 2001US-00946374.
15-JAN-2002; 2002US-00052586.
(GETH) GENENTECH INC.
Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
WPI; 2003-332034/31.
P-PSDB; ABU6251.
Three hundred and five nucleic acids encoding PRO polypeptides, useful in
gene therapy, chromosome identification, tissue typing, and for detecting
the presence of tumor in a mammal.
Claim 2; Fig 117; 707pp; English.
The invention relates to three hundred and five nucleic acids encoding
PRO polypeptides (secreted and transmembrane), sequences 80% identical to
them, or encoding a PRO polypeptide lacking its associated signal peptide
or an extracellular domain of the PRO polypeptide, with or lacking its
associated signal peptide. Also included are the encoded PRO proteins,
PRO expression vectors, host cells transformed with the vector (used to
produce PRO proteins), a chimeric molecule comprising the PRO
polypeptide fused to a heterologous amino acid sequence, an anti-PRO
antibody, a method for stimulating the release of tumor necrosis factor
alpha (TNF-alpha) from human blood (by contacting the blood with PRO1079,
PRO827, PRO791, PRO1131, PRO1183, PRO1343, PRO1760, PRO1567 or
PRO4333), a method for stimulating the proliferation or differentiation
of chondrocyte cells by contacting the cells with a PRO6029 polypeptide,
a method for detecting the presence of tumour in a mammal and an
oligonucleotide probe derived from any of the nucleotide sequences cited
above. The PRO polypeptide or anti-PRO antibody is useful for preparing a
medicament for treating a condition that is responsive to the PRO
polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful
as hybridisation probes in chromosome and gene mapping, or in generating
antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO
polypeptides, in assays to identify other proteins or molecules involved
in a binding reaction, to generate transgenic animals or knockout
animals, which in turn are useful in the development and screening of
therapeutically useful reagents, for chromosome identification, and
tissue typing. The PRO polypeptides and nucleic acid molecules are also
useful for detecting the presence of a tumour in a mammal, stimulating the
proliferation or differentiation of chondrocyte cells, stimulating the
release of tumour necrosis factor-alpha from human blood, in gene
therapy, or as molecular weight markers for protein electrophoresis
purposes. The anti-PRO antibodies may be used in diagnostic assays for
-PRO, or for the affinity purification of PRO from recombinant cell
culture or natural sources. The present sequence is a cDNA encoding a PRO
protein

Seq	Sequence	2764 BP; 689 A; 798 C; 717 G; 560 T; 0 U; 0 Other;
Query Match	70.2%;	Score 1078.8; DB 8; Length 2764;
Best Local Similarity	81.4%;	Pred. No. 9.3e-291;
Matches 1329; Conservative	0;	Mismatches 207; Indels 96; Gaps 3;
Qy	1	ATGCTACTGCCACTGCTGCTGCTCTGCTGCTGGCGGGTCCAGGCTATGGATGGGAGA 60
Db	46	ATGCTACTGCCACTGCTGCTCTGCTGCTGGCGGGTCCAGGCTATGGATGGGAGA 105
Qy	61	TTCTGTGATACGAGTCAGGAGTCAGTGATGGTSCCGGAGGGCTGTGCATCTCTGTGCC 120
Db	106	TTCTGTGATACGAGTCAGGAGTCAGTGATGGTSCCGGAGGGCTGTGCATCTCTGTGCC 165
Qy	121	TGCTCTTTCTCTACCCCCACAGGACTGGACAGGCTTACCCAGCTTATGCTACTGG 180
Db	166	TGCTCTTTCTCTACCCCCACAAGACTGGACAGGCTTACCCAGCTTATGCTACTGG 225
Qy	181	TTCAAAGCAGTACTGAGACACCAAGAGTGTCTGTGGCCACAACACCAAGGGAAC 240
Db	226	TTCAAAGCAGTACTGAGACACCAAGAGTGTCTGTGGCCACAACACCAAGGGAAC 285
Qy	241	GAGTGGAAATGAGCACCCGGGGCCGATTCAGCTCACTGGGGATCCCGCAAGGGAAC 300
Db	286	GAGTGGAAATGAGCACCCGGGGCCGATTCAGCTCACTGGGGATCCCGCAAGGGAAC 345
Qy	301	TGCTCTTTGGTGTATCAGACACGGCAGATGCAGGATGAGTCACAGTACTTTCGGGTG 360
Db	346	TGCTCTTTGGTGTATCAGACACGGCAGATGCAGGATGAGTCACAGTACTTTCGGGTG 405
Qy	361	GAGAGAGGAAGCTATGTGAGATATATTTTCATGAACGATGGGTCTTTCTTAAAGTAACA 420
Db	406	GAGAGAGGAAGCTATGTGAGATATATTTTCATGAACGATGGGTCTTTCTTAAAGTAACA 465
Qy	421	GCCTTGACTCAGAGGCTGATGTCTACATCCCGGAGACC----- 459
Db	466	GTGCTCAGCTTTCAGCGCCAGACCCCAAGGACCAACACCGACCTCACCCTGATGGAC 525
Qy	460	-----CTGGAGCCCGGCGACGCGGTGACGCT 485
Db	526	TTCTCCAGAAAGGTGTGAGCGCACAGAGGACCGTCCGACTCGTGTGGCCTATGCCCC 585
Qy	486	CATCTGTGTTTAACTGGGCTTTGAGAAATGTCCACCCCTTTCTTCTCTGGACGGG 545
Db	586	AGAGACCTTGTTATCAGCATTTTCAGTGACACACGCCAGCCTGGAGCCCCAGCCCCAG 645
Qy	546	GGCTGCCCTCTCCTCCAGGAACCAACACGACCTCCCACTTCTCAGTGCTCAGCTT 605
Db	646	GGAATATGCCATACCTCTGAAAGCCCAAAAGGCGAGTTCTCTGGGCTCTCTGTGTGCT 705
Qy	606	CAGCCCCAGACCCCAAGGACCCAC-----GACACCCACCTCAC 641
Db	706	GACAGCACCCCTCTGCCACACTGAGCTGGGTCTTGACGACAGAGTCTCTCTCTCGTCC 765
Qy	642	CTGCCATGTGGATCTCTCAGAAAGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGT 701
Db	766	CATCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGTGAAGCTGGGGATTCA 825
Qy	702	GGCCTATGCCCCACAGAGACTTGTATCAGCATTTTCAGTGACCAACACGCC----- 752
Db	826	GGGCGCTACACCTGCCGACGGGAGACAGGCTTGCTCCAGACGAGCCCTTGGACCTC 885
Qy	753	-----AGATCCTCCAGAGAACCTGAGAGTGTATGGTTTCCAGCAACAGGACAGTCC 804
Db	886	TCTGTGCATATCTCCAGAGAACCTGAGAGTGATGGTTTCCAGCAACAGGACAGTCC 945
Qy	805	CTGGAAACCTTTGGGAAAGGCGAGTCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCCCTG 864
Db	946	CTGGAAACCTTTGGGNAAGGCGAGTCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCCCTG 1005
Qy	865	GTCTGTGTCAACACAGCAGCCCCCAGCCAGCTGAGCTGACCCAGAGGGGACAGGTTT 924
Db	1006	GTCTGTGTCAACACAGCAGCCCCCAGCCAGCTGAGCTGAGTGAACCCAGAGGGGACAGGTTT 1065

925	CTGAGCCCTCCAGAGCCCTCAGACCCCGGGGTCTCTGGAGCTGCTCGGGTTCAGGTGGAG	984
1066	CTGAGCCCTCCAGAGCCCTCAGACCCCGGGGTCTCTGGAGCTGCTCGGGTTCAGGTGGAG	1125
985	CACGAAGGAGAGTTACCTGCGACGCTCGGCACCGACTGGGTCCAGACAGGTCCTCTC	1044
1126	CACGAAGGAGAGTTACCTGCGACGCTCGGCACCGACTGGGTCCAGACAGGTCCTCTC	1185
1045	AGCCTCTCGTGACATATGAAGGGACATCATCTAACGGCATTTCCAAATGGAGCGTTT	1104
1186	AGCCTCTCGTGACATATGAAGGGACATCATCTAACGGCATTTCCAAACGGAGCGTTT	1245
1105	CTGGGAATCGGATCAGGCTCTTTCTTCTCTGCTGCTGGCCCTGATCATCATGAAGATT	1164
1246	CTGGGAATCGGATCAGGCTCTTTCTTCTCTGCTGCTGGCCCTGATCATCATGAAGATT	1305
1165	CTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGCCACAGGTTCTCCGGCACAGCACG	1224
1306	CTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGCCACAGGTTCTCCGGCACAGCACG	1365
1225	ATCCTGGATTACATCAATGTGTTCCGAGCGCTGGCCCTCGCTCAGAAAGCGGAATCAG	1284
1366	ATCCTGGATTACATCAATGTGTTCCGAGCGCTGGCCCTCGCTCAGAAAGCGGAATCAG	1425
1285	AAAGCCACACCAACACAGTCTCGAGCCCTCTTTCCACAGGTGCTCCCTCCCGAGAAATCA	1344
1426	AAAGCCACACCAACACAGTCTCGAGCCCTCTTTCCACAGGTGCTCCCTCCCGAGAAATCA	1485
1345	AAGAAGAACAGAAAGACAGTATCAGTTGCCAGTTTCCACAGCCCAAAATCATCCACT	1404
1486	AAGAAGAACAGAAAGACAGTATCAGTTGCCAGTTTCCACAGCCCAAAATCATCCACT	1545
1405	CAAGCCCCAGAATCCAGGAGAGCCAGAGGAGCTCCATTATGCCAGCTCAACTTCCCA	1464
1546	CAAGCCCCAGAATCCAGGAGAGCCAGAGGAGCTCCATTATGCCAGCTCAACTTCCCA	1605
1465	GGCGTCAGACCCAGGCTGAGGCCCGGATGCCCAAGGGCACCCAGCGGATTATGCAGAA	1524
1606	GGCGTCAGACCCAGGCTGAGGCCCGGATGCCCAAGGGCACCCAGCGGATTATGCAGAA	1665
1525	GTCAAGTTCCAA	1536
1666	GTCAAGTTCCAA	1677

RESULT 9
ACA05758
ACA05758 standard; cDNA; 2764 BP.

ACA05758;

29-MAY-2003 (first entry)

Human secreted/transmembrane protein (PRO) cDNA #59.

XX Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
 KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
 KW tissue typing.

AA OS Homo sapiens.

XX-
-PN: US2003036162-A1.

20-FEB-2003.

12-JUL-2002: 2002US-00194423.

26-JUN-1998: 98US-00105413.

16-SEP-1998; 98WD-US019330;
07-OCT-1998; 98US-00168978;

07-OCT-1998; 98WD-US021141;
06-NOV-1998; 98US-Q0187368;

PR	01-DEC-1998;	98W0-US025108;
PR	07-DEC-1998;	98U5--00200504;
PR	03-MAR-1999;	99U5--00254311;
PR	14-MAY-1999;	99W0-US005028;
PR	08-NAR-1999;	99U5--00311832;
PR	12-JUN-1999;	99W0-US010733;
PR	04-SEP-1999;	99W0-US012252;
PR	25-AUG-1999;	98U5--00380137;
PR	25-AUG-1999;	98U5--00380138;
PR	25-AUG-1999;	99U5--00380139;
PR	25-AUG-1999;	99U5--00380142;
PR	01-SEP-1999;	99W0-US020111;
PR	18-OCT-1999;	99U5--00403297;
PR	15-SEP-1999;	99U5--00403297;
PR	12-NOV-1999;	99U5--00423844;
PR	01-DEC-1999;	99W0-US028301;
PR	02-DEC-1999;	99W0-US028551;
PR	03-DEC-1999;	99W0-US031274;
PR	05-JAN-2000;	2000W0-US000219;
PR	18-FEB-2000;	2000W0-US000341;
PR	18-FEB-2000;	2000W0-US004342;
PR	24-FEB-2000;	2000W0-US004414;
PR	24-FEB-2000;	2000W0-US005004;
PR	01-MAR-2000;	2000W0-US005601;
PR	02-MAR-2000;	2000W0-US005841;
PR	15-MAR-2000;	2000W0-US006894;
PR	30-MAR-2000;	2000W0-US008439;
PR	17-MAY-2000;	2000W0-US013705;
PR	22-MAY-2000;	2000W0-US014042;
PR	30-MAY-2000;	2000W0-US014941;
PR	02-JUN-2000;	2000W0-US015264;
PR	28-JUL-2000;	2000W0-US020710;
PR	22-AUG-2000;	2000U5--00644848;
PR	24-AUG-2000;	2000W0-US0232328;
PR	18-SEP-2000;	2000U5--00664610;
PR	18-SEP-2000;	2000U5--00665350;
PR	08-NOV-2000;	2000U5--00709238;
PR	08-NOV-2000;	2000W0-US030952;
PR	01-DEC-2000;	2000W0-US032678;
PR	20-DEC-2000;	2000U5--00747259;
PR	28-FEB-2001;	2000W0-US034956;
PR	28-FEB-2001;	2001W0-US0066520;
PR	02-MAR-2001;	2001U5--00816744;
PR	10-MAY-2001;	2001U5--00854208;
PR	10-MAY-2001;	2001U5--00854280;
PR	25-MAY-2001;	2001U5--00866028;
PR	01-JUN-2001;	2001W0-US017800;
PR	05-JUN-2001;	2001U5--00874503;
PR	20-JUN-2001;	2001W0-US019692;
PR	09-JUL-2001;	2001W0-US021066;
PR	29-JUL-2001;	2001W0-US021735;
PR	18-JUL-2001;	2001U5--00908827;
PR	30-JUL-2001;	2001U5--00918595;
PR	06-AUG-2001;	2001U5--00924410;
PR	13-AUG-2001;	2001U5--00925404;
PR	16-AUG-2001;	2001U5--00931836;
PR	28-AUG-2001;	2001U5--00941992;
PR	29-AUG-2001;	2001W0-US0207099;
PR	04-SEP-2001;	2001U5--00946374;
PR	15-JAN-2002;	2002U5--00052596;

(GETH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL; Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPT: 2003-332039/31

P-PSDB; ABU67464.

New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification.

ACA66592;
23-JUN-2003 (first entry)
cDNA encoding human PRO protein #59.
Human; tumour; adrenal; lung; colon; breast; prostate; rectal; cervical;
liver; PRO; Gene therapy; Gene; ss.
Homo sapiens.
US2003036137-A1.
20-FEB-2003.
27-JUN-2002; 2002US-00184640.
26-JUN-1998; 98WO-00105413.
16-SEP-1998; 98WO-US019330.
07-OCT-1998; 98US-00168978.
07-OCT-1998; 98WO-US021141.
06-NOV-1998; 98US-00187368.
01-DEC-1998; 98WO-US025108.
07-DEC-1998; 98US-00202054.
03-MAR-1999; 99US-00254311.
08-MAR-1999; 99WO-US005028.
14-MAY-1999; 99US-00311832.
14-MAY-1999; 99WO-US010733.
02-JUN-1999; 99WO-US012252.
25-AUG-1999; 99US-00380137.
25-AUG-1999; 99US-00380138.
25-AUG-1999; 99US-00380139.
25-AUG-1999; 99US-00380142.
01-SEP-1999; 99WO-US020111.
15-SEP-1999; 99WO-US021090.
18-OCT-1999; 99US-00403297.
12-NOV-1999; 99US-00423844.
01-DEC-1999; 99WO-US028301.
02-DEC-1999; 99WO-US028551.
30-DEC-1999; 99WO-US031274.
05-JAN-2000; 2000WO-US000219.
18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004342.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US005004.
01-MAR-2000; 2000WO-US005601.
02-MAR-2000; 2000WO-US005841.
15-MAR-2000; 2000WO-US006894.
30-MAR-2000; 2000WO-US006839.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US020710.
22-AUG-2000; 2000US-00644848.
24-AUG-2000; 2000WO-US023328.
18-SEP-2000; 2000US-00664610.
18-SEP-2000; 2000US-00665350.
08-NOV-2000; 2000US-00709238.
08-NOV-2000; 2000WO-US030952.
01-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000US-00747259.
20-DEC-2000; 2000WO-US034956.
28-FEB-2001; 2001WO-US006520.
22-MAR-2001; 2001US-00816744.
10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854280.
25-MAY-2001; 2001US-00856028.
01-JUN-2001; 2001WO-US017800.
05-JUN-2001; 2001US-00874503.
20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.

ACA66592;
23-JUN-2003 (first entry)
cDNA encoding human PRO protein #59.
Human; tumour; adrenal; lung; colon; breast; prostate; rectal; cervical;
liver; PRO; Gene therapy; Gene; ss.
Homo sapiens.
US2003036137-A1.
20-FEB-2003.
27-JUN-2002; 2002US-00184640.
26-JUN-1998; 98US-00105413.
16-SEP-1998; 98WO-US019330.
07-OCT-1998; 98US-00168978.
07-OCT-1998; 98WO-US021141.
06-NOV-1998; 98US-00187368.
01-DEC-1998; 98WO-US025108.
07-DEC-1998; 98US-00202054.
03-MAR-1999; 99US-00254311.
08-MAR-1999; 99WO-US005028.
14-MAY-1999; 99US-00311832.
14-MAY-1999; 99WO-US010733.
02-JUN-1999; 99WO-US012252.
25-AUG-1999; 99US-00380137.
25-AUG-1999; 99US-00380138.
25-AUG-1999; 99US-00380139.
25-AUG-1999; 99US-00380142.
01-SEP-1999; 99WO-US020111.
15-SEP-1999; 99WO-US021090.
18-OCT-1999; 99US-00403297.
12-NOV-1999; 99US-00423844.
01-DEC-1999; 99WO-US028301.
02-DEC-1999; 99WO-US028551.
30-DEC-1999; 99WO-US031274.
05-JAN-2000; 2000WO-US000219.
18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004342.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US005004.
01-MAR-2000; 2000WO-US005601.
02-MAR-2000; 2000WO-US005841.
15-MAR-2000; 2000WO-US006894.
30-MAR-2000; 2000WO-US006839.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US020710.
22-AUG-2000; 2000US-00644848.
24-AUG-2000; 2000WO-US023328.
18-SEP-2000; 2000US-00664610.
18-SEP-2000; 2000US-00665350.
08-NOV-2000; 2000US-00709238.
08-NOV-2000; 2000WO-US030952.
01-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000US-00747259.
20-DEC-2000; 2000WO-US034956.
28-FEB-2001; 2001WO-US006520.
22-MAR-2001; 2001US-00816744.
10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854280.
25-MAY-2001; 2001US-00856028.
01-JUN-2001; 2001WO-US017800.
05-JUN-2001; 2001US-00874503.
20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.

Db 466 GTGCTCAGCTTCAGGCCAGACCCAGGACCAACACACGACGACCTCACCTGCTCATGTGGAC 525
Qy 460 -----CTGGAGCCCGGGAGCGCCGCTGACGGT 485
Db 526 TTCTCCAGAAAGGTGTGACGACAGAGACCGTCCGACTCGCTGTGGCTATGCCCC 585
Qy 486 CATCTGTGTGTTAACTGGGCTTTGAGGAATGTCACCCCTCTTTCTCTGGACGGG 545
Db 586 AGAGACCTTGTATCAGCATTTTCAGGTGACACACGCGGCTTGAGCCCGACGCCAG 645
Qy 546 GGCTGCCCTCTCTCCCAAGAAACCAACCAAGACTTCCCACTTCTCAGTGTCTAGCTT 605
Db 646 GGAATGTCCCATACCTCTGGAAGCCCAAAAGGCGAGTTCCTGGGCTCTCTGTGTCT 705
Qy 606 CAGCCCGACAGCCCGAGGACAC-----GACACGACCTCAC 641
Db 706 GACAGCCAGCCCTGCCACACTGAGCTGGGTCTGACAGACAGATCTCTCTCTGTC 765
Qy 642 CTGCCATGTGGACTTCTCCAGAAGGGTGTGACGACAGAGACCGTCCGACTCGGTGT 701
Db 766 CATCTCTGGGCTGTAGACCCCTGGGCTGAGCTGCCGGGTGAAGCTGGGGATTCA 825
Qy 702 GGCTATGCCCCCAGAGACCTTGTATCAGCATTTACGTGACAAACACGCC-----752
Db 826 GGGGCTACCTGCGAGCGGAGAACAGCTTGGCTCCAGCAGCGGCTTGACCTC 885
Qy 753 -----AGATCCTCCAGAGAACCTCAGAGTGTGTTTCCCAAGCAACAGGACGTC 804
Db 886 TCTGTGCAGTATCTCCAGAGAACCTGAGAGTGTGTTTCCCAAGCAACAGGACAGTC 945
Qy 805 CTGGAACCTTGGGAACGCACTCTCTCCAGTACTGAGGCGCAAGCTGTGCTCTG 864
Db 946 CTGGAACCTTGGGAACGCACTCTCTCCAGTACTGAGGCGCAAGCTGTGCTCTG 1005
Qy 865 GTCTGTGTACACACAGCAGCCCGCCAGCCAGCTGAGTGGACCCAGAGGGACAGGTT 924
Db 1006 GTCTGTGTACACACAGCAGCCCGCCAGCCAGCTGAGTGGACCCAGAGGGACAGGTT 1065
Qy 925 CTGAGCCCTTCCAGCCCTCAGACCCCGGGGCTCTGAGTGGCTCGGTTCAAGTGGAG 984
Db 1066 CTGAGCCCTTCCAGCCCTCAGACCCCGGGGCTCTGAGTGGCTCGGTTCAAGTGGAG 1125
Qy 985 CAGAGAGGAGTTACCTGCCAGCTCGGCACCCACTGGGCTCCAGACGCTCTCTC 1044
Db 1126 CAGAGAGGAGTTACCTGCCAGCTCGGCACCCACTGGGCTCCAGACGCTCTCTC 1185
Qy 1045 AGCCTCTCGTGCATATAAGAGGAGTCTATCTCAACGGCAATCTCCCAATGGAGGTTT 1104
Db 1186 AGCCTCTCGTGCATATAAGAGGAGTCTATCTCAACGGCAATCTCCCAACGGAGGTTT 1245
Qy 1105 CTGGGAATCGGCATCAGGCTCTTCTTCTCTGCTGGCCCTGATCATATGAAGTT 1164
Db 1246 CTGGGAATCGGCATCAGGCTCTTCTTCTCTGCTGGCCCTGATCATATGAAGTT 1305
Qy 1165 CTACCGAAGAGCGGACTCAGACAGAAACCCCGAGGCCAGGTTCTCCCGGCACAGCAG 1224
Db 1306 CTACCGAAGAGCGGACTCAGACAGAAACCCCGAGGCCAGGTTCTCCCGGCACAGCAG 1365
Qy 1225 ATCTCGATTACATCAATGTGTCGAGCGCTGGCCCTCGCTCAGAGCGGAATCAG 1284
Db 1366 ATCTCGATTACATCAATGTGTCGAGCGCTGGCCCTCGCTCAGAGCGGAATCAG 1425
Qy 1285 AAAGCCACACCAACAGTCTCGGACCTCTTTCACACAGGTGCTCCCTCCCGCAATCA 1344
Db 1426 AAAGCCACACCAACAGTCTCGGACCTCTTTCACACAGGTGCTCCCTCCCGCAATCA 1485
Qy 1345 AAGAGAAACAGAAAGAGTATCAGTTGCCAGTTTCCAGAACCCCAATCATCCACT 1404
Db 1486 AAGAGAAACAGAAAGAGTATCAGTTGCCAGTTTCCAGAACCCCAATCATCCACT 1545
Qy 1405 CAGGCCCCAGATCCAGAGGAGCCAGAGGAGTCCATTATGCCAGCTCAACTTCCCA 1464
Db 1546 CAGGCCCCAGATCCAGAGGAGCCAGAGGAGTCCATTATGCCAGCTCAACTTCCCA 1605

Qy 1465 GCGCTCAGACCCAGCGCTGAGCCCGGATGCCAAGGCAAGGCAAGGCGGATATCGAGAA 1524
Db 1606 GCGCTCAGACCCAGCGCTGAGCCCGGATGCCAAGGCAAGGCAAGGCGGATATCGAGAA 1665
Qy 1525 GTCAAGTTCCAA 1536
Db 1666 GTCAAGTTCCAA 1677

RESULT 11
ACF20167

ID ACF20167 standard; cDNA; 2764 BP.

XX ACF20167;

XX DT 18-SEP-2003 (first entry)

XX Human secreted polypeptide PRO940-encoding cDNA, SEQ ID NO:117.

DE KW Human; PRO; secreted protein; transmembrane protein;
EX KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy; gene; ss.

OS Homo sapiens.

XX US2003040063-A1.

XX PD 27-FEB-2003.

XX PF 26-JUN-2002; 2002US-00183006.

XX PR 18-SEP-1997; 97US-0059263P.

XX PR 18-SEP-1997; 97US-0059266P.

XX PR 17-OCT-1997; 97US-0062250P.

XX PR 21-OCT-1997; 97US-0063486P.

XX PR 24-OCT-1997; 97US-0063120P.

XX PR 24-OCT-1997; 97US-0063121P.

XX PR 28-OCT-1997; 97US-0063540P.

XX PR 28-OCT-1997; 97US-0063541P.

XX PR 28-OCT-1997; 97US-0063544P.

XX PR 29-OCT-1997; 97US-0063734P.

XX PR 31-OCT-1997; 97US-0063870P.

XX PR 31-OCT-1997; 97US-0064103P.

XX PR 13-NOV-1997; 97US-0065311P.

XX PR 21-NOV-1997; 97US-0066120P.

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XX PR 10-MAR-1998; 98US-0077450P.

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XX PR 15-APR-1998; 98US-0081888P.

XX PR 21-APR-1998; 98US-0082568P.

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RESULT 12
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ID ACFI9553 standard; cDNA; 2764 BP.
XX AC ACFI9553;
XX DT 17-SEP-2003 (first entry)
XX DE Human secreted polypeptide PRO940-encoding cDNA, SEQ ID NO:117.
XX KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy; gene; ss.
XX OS Homo sapiens.
XX PN US2003040064-A1.
XX PD 27-FEB-2003.
XX PF 26-JUN-2002; 2002US-00183008.
XX PR 18-SEP-1997; 97US-0059263P.
XX PR 18-SEP-1997; 97US-0059266P.
XX PR 17-OCT-1997; 97US-0062250P.
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us-09-937-636-1.rng

XX	Human secreted/transmembrane protein (PRO) cDNA #59.	PR	28-MAY-1998;	98US-0087098P.
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XX	prostate tumour; rectal tumour; cervical tumour; liver tumour.	PR	03-JUN-1998;	98US-0087827P.
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XX		PR	18-AUG-1998;	98US-0096949P.
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us-09-937-636-1.rng

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1666 GTCAGTTCCAA 1677

RESULT 14

ACFI3006

ACFI3006 standard; cDNA; 2764 BP.

ACFI3006;

13-SEP-2003 (first entry)

Human secreted polypeptide PRO940-encoding cDNA, SEQ ID NO:117.

Human; PRO; secreted protein; transmembrane protein;
extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
Chondrocyte; proliferation; differentiation; cartilage disorder;
bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
liver; drug screening; transgenic animal; genetic analysis;
antiarthritic; vulnery; gene therapy; gene; ss.

Homo sapiens.

US2003036160-A1.

20-FEB-2003.

02-JUL-2002; 2002US-00188791.

18-SEP-1997; 97US-0059263P.
18-SEP-1997; 97US-0059266P.
17-OCT-1997; 97US-0063250P.
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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
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GenCore version 5.1.6
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Listing first 45 summaries

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ALIGNMENTS

RESULT 1

US-09-038-832-3

; Sequence 3, Application US/09038832

; Patent No. 6146845

; GENERAL INFORMATION:

; APPLICANT: KIKLY, KRISTINE

; APPLICANT: BRICKSON-MILLER, CONNIE

; TITLE OF INVENTION: Sialoadhesin Family Member-2

; TITLE OF INVENTION: (SAF-2)

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA: US/09/038,832

; APPLICATION NUMBER: US/09/038,832

; FILING DATE: 11-MAR-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/041,886

; FILING DATE: 02-APR-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GH-50018

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0701

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1597 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-09-038-832-3

Query Match 23.8%; Score 364.8; DB 3; Length 1597;
Best Local Similarity 62.1%; Pred. No. 3.1e-96;
Matches 666; Conservative 0; Mismatches 337; Indels 3;

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; Patent No. 6146845
; GENERAL INFORMATION:
; APPLICANT: KIRLY, KRISTINE
; APPLICANT: ERICKSON-MILLER, CONNIE
; TITLE OF INVENTION: Staloesin Family Member-2
; TITLE OF INVENTION: (SAF-2)
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,832
; FILING DATE: 11-MAR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,886
; FILING DATE: 02-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-038-832-1

Query Match 23.8%; Score 364.8; DB 3; Length 2900;
Best Local Similarity 62.1%; Pred. No. 4.1e-96;
Matches 666; Conservative 0; Mismatches 337; Indels 69; Gaps 3;
QY 59 GATTCTGATACAGTGCAGGAGTCAAGTGTGTCGGAGGGCTGTGCATCTCTGTGC 118
DB 137 GTTACTTGTCTGCAAGTGCAGGAGTGTGACGTGTGAGGAGGGCTGTGTCTCAATGTGC 196
QY 119 CTTCTCTTCTCTTACCCCGACAGACTGTGACAGGGTCTACCCAGCTTATGGCTACT 178
DB 197 CTTCTCTTCTCTTACCCCGACAGACTGTGACAGGGTCTACCCAGCTTATGGCTACT 256
QY 179 GGTTCAGAGAGTCTGAGACACCAAGAGTGTCTCTGTGGCCACAAACCCAGAGTC 238
DB 257 GGTTCGGGCHAGAGACAGACCATACCAAGAGTGTGAGGGTCAATATCTTTCGGC 316
QY 239 GAGAGGTGGAATGAGACACCGGGCGGATTCAGAGTCTACCTGAGGATTCGGGCAAGGGA 298
DB 317 GAGAAGTGCAGGACAGACCCAGGGCGGATTCAGAGTCTACCTGAGGATTCGGGCAAGG 376
QY 299 ACTGCTCTTGTGATCAGAGAGCGGAGATGCAGAGTGTGACAGTCTCTTTCGGG 358
DB 377 ACTGCTCTTGTGATCAGAGAGCGGAGATGCAGAGTGTGAGGATTCAGAGTGTGAGG 436
QY 359 TGGAGAGGAGGAGCT-----ATGTGAGATATAATTTTCATGAACGATGGGT 403
DB 437 TAGAGAGAGGAGGAGCTTTACAAATCAGTGTGAATTTACAAACTAAGCAGC 496

404 TCTTTCTAAAGTAACAGCCCTGACTCAGAAAGCTGATGCTATACATCCCGAGACCCCTGG 463
Db TGCTGTGTTGTGACAGCCCTGACCAATAGGCTGACATCTCTATCTCTAGGACCCCTAG 556
464 AGCCCGGACCGGTGACGGTCTATGCTGTGTTAACTGGGCTTTGAGGAATGCCAC 523
Db AGTCTGCCACTCAGGAACCTGACCTGCTGTGCCCTGGGCTGTAAAGCAGGGGACAC 616
524 CCCTCTTTCTCTGACCGGGGCTGCCCTCTCTCCCAAGGAACCAACCAACGACCT 583
Db CCCCCTGATCTCTGGATGGGCTCGCTGTCTCCCGGGCCCTCCCTACTACTG 670
584 CCACCTTCTGAGTCTGCTCAGCTTACGCCGACAGCCAGGACCAAGGACCTGACCT 643
Db CCGCTCTCTGAGTCTGCTCAGCTTACCCCAAGGCTCCAGGACCAAGGACCTGACCT 730
644 GCATGTGGACTCTCCAGAAAGGTGTGACGCGACAGAGGACCGTCCGACTCCGTGTGG 703
Db GTGAGTGTGCTGCTGGACAGGTGTGACCAAGGACCTGACCTGCTCCGCTGATGTGT 790
704 CTTATGCCCCAGAGACCTTGTATCAGCATTTTCACTGTGACAAACAGCCAGATCTCCAG 763
Db CTT CCT-----ACCTCTCT 802
764 AGAACCTGAGAGTGTGTTTCCCAAGCAACAGGACAGTCTCTGAAACCTTTGGAAAG 823
Db GGAACCTGACATGATGCTTCAAGGAGATGCCAGCATCCAGCCCTGGGAATG 862
824 GCAGCTCTCCAGTACTGAGGGGCAAGCCGTGCTGCTGCTGTGTGTACACAGCA 883
Db GCTCATCTCTTCACTGCTTGAAGGCGAGTCTCTGGGCTGTGTGTGTCAACAGCA 922
884 GCGCCCGACGAGCTGAGTGTGACCCAGAGGGGACAGGTCTGAGCCCTCCAGCCCT 943
Db ATCCCCCTGACGCTGAGTGTGACCCGGGGAGCTTGCCTGTGCTGCTGCTGCTGCT 982
944 CAGACCCCGGGGCTCTGGAGTCTGCTCGGCTTCAAGTGGAGCAGCAAGGAGATTCACCT 1003
Db CAACCTCTGGCTCTGGAGTCTGCTGAGTGTGACGCTGAGGGATGAAGGGGATTCACCT 1042
1004 GCACGCTCGGACCCCTAGCTGGCTCCAGCAGCTCTCTCTGACCTCTCGGTGCTATTA 1063
Db GCGAGCTCAGAGCTGAGGCTGAGGCTCCAGCAGCATTTCCCTGAGCTCTCCCTGAGATG 1102
1064 AGAAGGAGCTCATCTCAACGGCTTCCCAATGAGGCTTCTGGAATCGG 1115
Db AGGCACAGGACCTCAAGACCTGTATCAGATGACACTGGCAGCAGTCCG 1154

RESULT 3

US-09-046-736-1
; Sequence 1, Application US/09046736
; Patent No. 6090582
; GENERAL INFORMATION:
; APPLICANT: KIRBY, KRISTINE
; APPLICANT: ERICKSON-MILLER, CONNIE
; TITLE OF INVENTION: Sialoadhesin Family Member-3
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,736

; FILING DATE: 24-MAR-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,885
; FILING DATE: 02-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1501 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-046-736-1

Query Match 21.6%; Score 332.4; DB 3; Length 1501;
Best Local Similarity 60.7%; Pred. No. 8.4e-87;
Matches 671; Conservative 0; Mismatches 366; Indels 69; Gaps 5;

QY 61 TTCTGATACGAGTGCAGAGTCTAGTGTGTCGGAGGCGCTGTGTCATCTCTGTGCC 120
Db TACTCGCTGAGATCAGAGTTCCTGACCGTGCAGAGGCGATGTGTCAATGTGCG 157
QY 121 TGCTCTTTCTCTATCCCCGACAGGACTGGAAGGGTCTACCCAGCTTATGGTACTGG 180
Db TGCTCTTTCTCTATCCCCGACAGGACTGGAAGGGTCTGACCCAGTCTGACCCAGTCTCATGGCTACTGG 217
QY 181 TTCAAAGCAGTGTGACAGCAACCAAGGGTCTCTGTGGCCACAACACCCAGAGTCGA 240
Db TTCCGGGAGGGAATGATATAGCTGGAAGGCTCCAGTGGCCACAACACCCAGCTGG 277
QY 241 GAGGTGGAATAGACACCCGGGGCGATTTCCAGTCTCACTGGGGATCCCGCCAAAGGGGAAAC 300
Db GCAGTGCAGGAGGAACCTCGGACCGATTTCCACCTCTCTGGGACCCACAGACCAAAAT 337
QY 301 TGCTCTTTGATGATCAGAGCGGAGATGAGGATGAGTACAGTACTTCTTTGGGTG 360
Db TGACCCCTGAGCATCAGAGATGCCAGATGATGATGGGGAGATCTTCTTTGATG 397
QY 361 GAGAGGAGAGCTATGTGAGATATAATTTCAATGACGATGGTCTTTCTAAAGTAACA 420
Db GAGAAAGGAA---ATATAAATGGAATTAATAATATGACAGCTCTCTGTGACGTGACA 454
QY 421 GCCCTGACTCAGAGCCCTGATGTCTATATCCCGAGACCCCTGGAGCCCGGGCAGCCGGTG 480
Db GCCTTGACCCACAGGCCCAACATCCTTATCCCGGTACCTGGAGTCTGGCTTCCAG 514
QY 481 ACGGTCACTGTGTGTTTAACTGGGCTTTGAGGAATGTCACCCCTTCTTCTCTCTGG 540
Db AATCTGACTGTCTGTGCTTGGGCTGTGAGCAGGGAGCGCCCCCTATGATCTCTCTGG 574
QY 541 ACGGGGGTGGCTCTCTCTCCCAAGGAACCAACCAAGCTTCCACTTTCTCACTGTCTC 600
Db ATGGGGACCTGTGTGCTCCCTCC---CGCACCCCTCCACCCCGCTCTCTCGGTGCTC 628
QY 601 AGCTTCAGCCCGACAGCCCGCAGGACCAAGACCCGCTCCTGACGATGTGACTTCTCC 660
Db ACCCTCATCCCCACAGCCCGCAGCACCACCGACCCAGCTCAGCTGTCAAGTACCTTGGCT 688
QY 661 AGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCTCCGTGGGCTATGCCCCCAGAGAC 720
Db GGGGCGGCGGTGACCAAGACAGGACCATCCAACTCAATGTCTCTAC----- 736
QY 721 CTTGTTATCAGCATTTACGTGACAAACAGGCGAGATCTCCAGAGAACTGAGAGTGTG 780
Db -----CCTCCTCAGAACTTGACTGTGACT 760

DB 73 TTCTGGCTGCAAGTGCAGGAGTCACTGACGCTACAGGAGGTTTGTGCGTCTCGTGGCC 132
QY 121 TGCTCTTTCTCCTACCCCGACAGGACTGGACAGGTTCTACCCAGGTTATGGCTACTGG 180
DB 133 TGCATTTCTTCCATCCATACCTACTACGACAGAACTCCGAGTTGATGGTACTGG 192
QY 181 TTCAAAGCAGTGAATGACAGAACCAAGGGTCTCTCTGGCCCAAAACCAACCCAGAGTCGA 240
DB 193 TTCGGGAAGGAGGCAATATATCCGGGCACTCTCCAGTGGCCCAAAACAAGCTAGATCAA 252
QY 241 GAGTGGAATGAGCACCCGGGCGGATCCAGCTCACTGGGATCCGCAAGGGGAAC 300
DB 253 GAAGTACAGGAGGAGACTCAGGGGAGATTCGGCTCTCTGGGATCCAGTAGGAACAC 312
QY 301 TGCTCTTTGGTGATCAGAGACGCGCAGATGACGAGTACAGTACTTCTTTGCGGTG 360
DB 313 TGCTCCCTGACATCGTAGAGCCGAGGAGGAGTAATGTTTCATATCTTTTCGGATG 372
QY 361 GAGAGAGAACTATGTGAGATATAATTTCAATGAACGATGGTTCTTTCTAAAGTAACA 420
DB 373 GAGAGAGGAAG---TACCAATACAGTTACAAATCTCCGAGCTCTCTGTGCAATGACA 429
QY 421 GCCCTGACTCAGAAACCTGTCTTACATCCCGAGACCCCTGGAGCCCGGCGAGCGGTG 480
DB 430 GACTTGACCCACAGGCCCAAAATCTCATCTCTGGCACTCTAGAACCAGGCACTCCAAA 489
QY 481 ACGGTATCTGTGTGTTAACTGGGCTTTGAGGAATGTCCACCCCTTTCTTCTCTGG 540
DB 490 AACCTTACTCTCTGTGTCTCTGGGCTGTGAGCAGGAAACACCCCGATCTTCTCTGG 549
QY 541 ACGGGGTGCTCTCTCTCCCAAGAACCAAAACCAACGACTCTCCACTTCTCAGTCTC 600
DB 550 TTGTGAGTGTGCT 603
QY 601 AGCTTACGCGCAGACCCAGGACACGACACGACCTCTCTCTCTCTCTCTCTCTCTCTCT 660
DB 604 ATAATCACCCACGCGCCCGGACGACGACGACGACGACGACGACGACGACGACGACG 663
QY 661 AGAAGGAGTGTGAGGACACGACGACGACGACGACGACGACGACGACGACGACGACG 720
DB 664 GGAGCTGTGTGACTACGAGAGAACATCCAGCTCAACGTCACCTATGTTCCACAGAAC 723
QY 721 CTGTGTATCAGATTTCACTGACACACGACGACGACGACGACGACGACGACGACGACG 780
DB 724 CCAACAACGTGTATCTTCCAGGAGATGGCTCAGGGAACCAAGAGACGAGCAGGACTG 783
QY 781 GTT 783
DB 784 GTT 786

RESULT 7

US-09-513-999C-3082
; Sequence 3082, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3082
; LENGTH: 192
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..192
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 12
; OTHER INFORMATION: s-g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 84
; OTHER INFORMATION: s-g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 105
; OTHER INFORMATION: s-g or c
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 28
; OTHER INFORMATION: Xaa=His or Gln
; US-09-513-999C-3082

Query Match 12.4%; Score 190.8; DB 4; Length 192;

Best Local Similarity 98.4%; Pred. No. 66-45; 0; Indels 0; Gaps 0;
Matches 189; Conservative 3; Mismatches 0

QY 391 ATGAACGATGGGTTCTTTCTAAAGTAACAGCCCTGACTCAGAACCTGATGTCTACATC 450
DB 1 ATGAACGATGGGTTCTTTCTAAAGTAACAGCCCTGACTCAGAACCTGATGTCTACATC 60
QY 451 CCGGAGACCTCGAGCCCGGGAGCCGGTACGCTCATCTGTGTGTTAACTGGGCTTT 510
DB 61 CCGGAGACCTCGAGCCCGGGAGCCGGTACGCTCATCTGTGTGTTAACTGGGCTTT 120
QY 511 GAGGATGTCCACCCCTTTCTTCTCTGGAGGGGCTGCCCTCTCTCCCAAGGAACC 570
DB 121 GAGGATGTCCACCCCTTTCTTCTCTGGAGGGGCTGCCCTCTCTCCCAAGGAACC 180
QY 571 AAACCAAGAAC 582
DB 181 AAACCAAGAAC 192

RESULT 8

US-09-046-736-3
; Sequence 3, Application US/09046736
; Patent No. 6090582
; GENERAL INFORMATION:
; APPLICANT: KIKLY, KRISTINE
; APPLICANT: ERICKSON-MILLER, CONNIE
; TITLE OF INVENTION: Sialoadhesin Family Member-3
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,736
; FILING DATE: 24-MAR-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,885
; FILING DATE: 02-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031

```

RESULT 9
US-09-513-999C-522
; Sequence 522, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 522
; LENGTH: 231
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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LOCATION: (310)..(310)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (325)..(325)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (328)..(328)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (331)..(331)
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LOCATION: (415)..(416)
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NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (421)..(421)
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NAME/KEY: misc feature
LOCATION: (428)..(431)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (434)..(434)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (436)..(436)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (438)..(439)
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NAME/KEY: misc feature
LOCATION: (442)..(443)
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NAME/KEY: misc feature
LOCATION: (445)..(445)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (449)..(450)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (459)..(459)

OTHER INFORMATION: May be any nucleotide
US-08-896-537A-11

Query Match 6.1%; Score 93.4; DB 4; Length 459;
Best Local Similarity 58.6%; Pred. No. 2.3e-17;
Matches 177; Conservative 0; Mismatches 124; Indels 1; Gaps 1;
QY 171 TGGCTACTGGTCAAGCAGTCTGACGACAAACCAAGGGTCTCTCTGGGCCCAAAACCA 230
DB 4 TCGGCANAGGTTCCGGGACGGGNAGATCCCATATCTACCTGAGGTGGGCCCAAAACCA 63
QY 231 CCAGAGTCGAGAGGTGGAAATGAGCACCCGGGGCGGATTCAGAGTCTCACTGGGGATCCGC 290
DB 64 CCCAGACAGAGAGTGAAGCCAGAGACCCAGGGCGGATTCCTCTGGGGATGTCA 123
QY 291 CAAGGGAACTGCTCTTGGTGATCAGAGACGGCGGATGAGAGTGTGACAGTACAGTACTT 350
DB 124 GAAGAAGAACTGCTCTCTGAGCATCGGAGATCCAGAAATGAGGACACGGGAAGCTATT 183
QY 351 CTTTCGGGTGGAGAGAGGAAGCTATGT-GAGATATAATTTTCAATGAAATGGGTTCTTTC 409
DB 184 CTTTCGGGTGGAGAGAGGAAGGATGTAAATAATATAGCTACCAACAGATAAGCTGAAT 243
QY 410 TAAAGTAAAGCCCTGACTCAGAAAGCTGTGTCTATCATCCCGAGACCTCGAGCCCG 469
DB 244 TGGAGGTGACAGCCCTGTATAGAGAAACCCGACATCCACTTTTGGAGCCTTTGGAGTTC 303
QY 470 GG 471
DB 304 GG 305

RESULT 11

US-09-621-976-15639/c
Sequence 15639, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 15639
LENGTH: 505
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-15639

Query Match 2.6%; Score 39.6; DB 4; Length 505;
Best Local Similarity 11.2%; Pred. No. 0.12;
Matches 42; Conservative 165; Mismatches 169; Indels 0; Gaps 0;
QY 272 AGCTACTGGGGATCCCGCAAGGGAAGTCTCTCTGGTGATCAGAGACGGCAGATGC 331
DB 397 RGMRCARGTGSWGSWGGYRMWGRMAAAKMRMAAAGGSGYCGMTSVTSCKMTGRKGS 338
QY 332 AGGATGAGTCAAGTACTTTTTCGGGTGGAGAGGAAGCTATGTGAGATATAATTCA 391
DB 337 MTKRKEMTYSGMWTSYKCTKTGKKYKWSKKTRWTCTSWRKYMMWMSWCMRSKMS 278
QY 392 TGAACGATGGGTCTTTTCTAAAGTAAACAGCCCTGACTCAGAACCTGATCTACATCC 451
DB 277 ARSWTMMVACWCMMSASAYRARRSMYARRSMRAGAWRARRKGRARRKGRARRKGR 218
QY 452 CCGAGACCTTGAGCCCGGCGGCGGTGACGGTCACTGTGTGTTTAACTGGGCGCTTTG 511
DB 217 SSMRMSAGKARMCRRWMSCRMYSYCMGSKMCRGTCAKMRVYARVAKRYASSMGKYM 158
QY 512 AGGAATGCCACCCCTTTCTTCTCTGGACGGGGGTGGCCCTCTCTCCCAAGGAACCA 571

QY 1078 TCACGGCAATTCCTCAATGAGCGTTTCTGGATCGGATCAAGCTCTCTTTTCCTC 1137
DB 386 GTACCGCGGTGGCGCTGGAGCGGTGATGTCCAACACACCTGGAGCTGGTCTAGGAC 445
QY 1138 TGCCTGGGCC 1147
DB 446 GCGCTGGGC 455

RESULT 15
US-09-252-991A-1196/c
Sequence 1196, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 1196
LENGTH: 1335
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1196

Query Match 2.5%; Score 38; DB 4; Length 1335;
Best Local Similarity 45.2%; Pred. No. 0.57;
Matches 140; Conservative 0; Mismatches 170; Indels 0; Gaps 0;
QY 838 GTACTGGAGGCCAAAGCCTGTGCTGGTCTGTGTCTACACACAGCAGCCGCCAGCCAGG 897
DB 804 GTGATCGTTCGACGAGATCCATGCCCTGGCGGCGAGCAAGCGCGCACCTGGCGCTG 745
QY 898 CTGAGCTGGACCCAGAGGGGACAGGTTCTGAGCCCTCCAGCCCTCAGACCCCGGGGTC 957
DB 744 TCGCTGGAGCGCTGCAGCGCTGTGTCGCGACCGCTGTGCGGATCGGGCTGTCCGCC 685
QY 958 CTGAGCTGCTCGCGGTTCAAGTGGAGCAGCAAGAGAGATTCACTGCCAGCTCGGCAC 1017
DB 684 ACGCAGAAACCGATCGAGAGGTCGCGGCTTCTCTCGCGCCAGCGGCAATCCGCGC 625
QY 1018 CCACCTGGGCTCCAGCAGCTCTCTCTAGCCCTCTCCGTGCACTATAAGAGGGGACTCATC 1077
DB 624 GATCGGCTCGCGGATCTCGACATCGGCTATACGCGCCCGCGACCTGGGATCGAG 565
QY 1078 TCACGGCAATTCCTCAATGAGCGTTTCTGGATTCGGATTCGGATTCAGGCTCTTTTCCTC 1137
DB 564 GTACCGCGGTGGCGCTGGAGCGGTGATGTCCAACGACACCTGGAGCTGGTCTAGGAC 505
QY 1138 TGCCTGGGCC 1147
DB 504 GCGCTGGGC 495

Search completed: November 8, 2004, 20:38:22
Job time : 173.477 secs

PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/084411
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084537
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084539
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084540
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
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PRIOR APPLICATION NUMBER: 60/085882

1	ATGCTACTGGCACA	CTGCTGCTGTCTT	CGCTGCTGGCGGGTCC	CAGAGCTATGATGGGAGA	60
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121	TGCTCTTTCTCCTAC	CCCCCGACAGGACT	TGGACAGGGTCTAC	CCCCAGTTATGGCTACTGG	180
166	TGCTCTTTCTCCTAC	CCCCCGACAGGACT	TGGACAGGGTCTAC	CCCCAGTTATGGCTACTGG	225
181	TTCAAAGCAGTGACT	TGACGACAAACAA	GGGTGCTCTGTGGCCACA	CAACACACAGAGTCGA	240
226	TTCAAAGCAGTGACT	TGACGACAAACAA	GGGTGCTCTGTGGCCACA	CAACACACAGAGTCGA	285
241	GAGGTGGAAATGAGCA	CCCGGGCGGATTC	CCAGCTCACTGGGATCCCC	CAAGGGGAAC	300
286	GAGGTGGAAATGAGCA	CCCGGGCGGATTC	CCAGCTCACTGGGATCCCC	CAAGGGGAAC	345
301	TGCTCTTTGGTGATC	CAGAGACCGCAGAT	TGCAGATGACAGTAC	AGTCACTTCTTCGGGTG	360
346	TGCTCTTTGGTGATC	CAGAGACCGCAGAT	TGCAGATGACAGTAC	AGTCACTTCTTCGGGTG	405
361	GAGAGGGAAGCTATG	TGCAGATATAATTT	CATGAACGATGGGTCTCT	TCTAAAGTAACA	420
406	GAGAGGGAAGCTATG	TGCAGATATAATTT	CATGAACGATGGGTCTCT	TCTAAAGTAACA	465
421	GGCCTGACTCAGAAG	CGTGATGTCTACAT	CTCCCGAGACC-----	-----	459
466	GTGCTCAGCTTCACG	CCCCAGACCCCGAGAC	CACAAACCCGACCTCACCT	TCACCTGCGATGTGGAC	525
460	-----	-----	-----	CTGGAGCCGGGACGCGGTGACGGT	485
526	TTCTCCAGAAAGGGTG	TGAGCGCACAGAGGAC	CGTCCGACTTCGTGTGGCCTAT	GCCCCC	585
486	CATCTGTGTGTTAACT	GGGCGTTTGAGGAAT	GTCCACCCGCTCTTTCT	CTCPGAGCGG	545
586	AGAGACCTTGTTTAT	CAGCATTTACGTTGAC	AAACACGCGCCCTTGGAGCC	CCACGCCAC	645
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646	GGAAATGTCCCATAT	CTTGAAGCCCAAAAG	GCCAGGTTCTGTGGGCTCTCT	GTGTGCTGT	705
606	CACGCCACACACCC	CAGGACCAAC-----	-----	GACACCGACCTCAC	641
706	GACAGCCAGCCCGCT	GCACACTGAGCTGGGTCT	CTGCAGAACAGAGTCTCT	CCTCGTCC	765
642	CTGCCATGTGGACTTCT	CCAGAAAGGGTGTGAG	CGCACAGAGGACCGTCCGACT	CCGCTGT	701
766	CATCCCTGGGGCCCT	TAGACCCCTGGGGCTG	GAGCTGGCCGGGGTGAA	GGCTGGGGATCA	825
702	GGCCTATGCCCCCAG	GAGACCTTGTTTATCAG	GATTTTCACTGACAAACGCGC	-----	752

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
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PRIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742

Query Match	70.24;	Score 1078.8;	DB 9;	Length 2764;	
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QY	61	TTCTGGATACAGATGACAGAGTCAAGTATGATGGTGC CGGAGGCGCTGTGATCTCTGTGCGCC	120		
DB	106	TTCTGGATACAGATGACAGAGTCAAGTATGATGGTGC CGGAGGCGCTGTGATCTCTGTGCGCC	165		
QY	121	TGCTCTTTCTCTACCCCGACAGGACTCGACAGGCTCTACCCAGCTTATGGCTACTGG	180		
DB	156	TGCTCTTTCTCTACCCCGACAGGACTCGACAGGCTCTACCCAGCTTATGGCTACTGG	225		
QY	181	TTCAAAGCAGTGACTGAGACAACCAAGGCTGCTCTGTGGGCAACAACACCCAGAGTCGA	240		
DB	226	TTCAAAGCAGTGACTGAGACAACCAAGGCTGCTCTGTGGGCAACAACACCCAGAGTCGA	285		
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DB	286	GAGGTGGAAATGAGCACCCGGGCGCGATTTCCAGCTCACTTGGGGATCCCGCCCAAGGGGAAC	345		
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DB	346	TGCTCTTTGGTGATCAGACGCGGAGATGCGAGGATGAGTCACAGTACTCTTTCGGGTG	405		
QY	361	GAGAGAGAAAGCTATGTGACATATAATTTTCATGAACGATGGGTCTTTCTAAAAAGTAACA	420		
DB	406	GAGAGAGAAAGCTATGTGACATATAATTTTCATGAACGATGGGTCTTTCTAAAAAGTAACA	465		
QY	421	GCCTTGACTCAGAAGCTGATGTCATACCTCCCGAGAC	459		
DB	466	GTGCTCAGCTTCAGCCCGACGCCAGGACCAACACCGACCTCACTGCCATGTGGAC	525		
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DB	536	TTCTCCAGAAAGGTGTGAGCGCACAGAGGACCGTCCGACTCCGCTGGCCCTATGCCCCC	585		
QY	486	CATCTGTGCTTTAACTGGGCTTTTGAAGAAATGCCACCCCTCTTTCTCTCGAGCGGG	545		
DB	586	AGAGACCTTTGTATCAGCATTTCACTGTGACACACGCCGAGCCCTGGAGCCCCAGCCCCAG	645		
QY	546	GGCTGCCCTCTCTCCCAAGGACCAACACGACCTCCCACTTCTCAGTGCTCAGCTT	605		
DB	646	GGAATGTCCCATACCTGGAAGCCCAAAAGGCCAGTTCTCTGGGCTCTCTGTGTGCTGT	705		

QY	606	CAGCCCGAGACCCAGAGACCAC-----GACACCGACCTCAC	641
Db	706	GACAGCCAGCCCGCTGCCACACTGAGCTGGGTCTCTGAGAACAGAGTCTCTCTCTCGTGCC	765
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QY	702	GGGCTATGCCCGCCAGAGACCTTGTATTACAGCATTTACGTGACAAACGCGC-----	752
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QY	753	-----AGATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAACACAGACAGTC	804
Db	886	TCTGTGCAGTATCTCTCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAACACAGACAGTC	945
QY	805	CTGAAACACCTTGGGAACGGCAGTCTCTCCCAGTACTGGAGGGCCAAAGCCCTGTGCCTG	864
Db	946	CTGGAACACCTTGGGAACGGCAGTCTCTCCAGTACTGGAGGGCCAAAGCCCTGTGCCTG	1005
QY	865	GTCTGTGTCTACACAGCAGCGCCCGCCAGCAGAGCTGAGCTGGACCCAGAGGGGACAGGTT	924
Db	1006	GTCTGTGTCTACACAGCAGCGCCCGCCAGCAGAGCTGAGCTGGACCCAGAGGGGACAGGTT	1065
QY	925	CTGAGCCCTTCCAGACGCTCAGACCCCGGGTCTCTGAGCTGCTCGGGTTCAAGTGGAG	984
Db	1066	CTGAGCCCTTCCAGACGCTCAGACCCCGGGTCTCTGAGCTGCTCGGGTTCAAGTGGAG	1125
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QY	1045	AGCTCTCCGTGCACTATAAGAGGGACTCATCTCAACGGCATTTCTCCAATGGAGCGTTT	1104
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QY	1105	CTGGGAATCGGCATCACGGCTCTTTTCTCTGCTGCGCCCTGATCATCAAGATT	1164
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QY	1165	CTACCGAAGAGCGGACTCAGACAGAAACCCGAGGCCAGGTTCTCCCGGCACAGCAGC	1224
Db	1306	CTACCGAAGAGCGGACTCAGACAGAAACCCGAGGCCAGGTTCTCCCGGCACAGCAGC	1365
QY	1225	ATCCTGGATTACATCAATGTGGTCCCGACCGCTGGCCCTCTGGCTCAGAAAGCGGAATCAG	1284
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QY	1285	AAAGCCACCAAAACAGTCTCGGACCGCTTCTTCCACAGGTGCTCCTCCCGAGAAATCA	1344
Db	1426	AAAGCCACCAAAACAGTCTCGGACCGCTTCTTCCACAGGTGCTCCTCCCGAGAAATCA	1485
QY	1345	AAGAAAGAACAGAAAGACGATATCAGTTGGCCAGTTTCCAGAAACCAAAATCATCCACT	1404
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QY	1405	CAAGCCCGAGAAATCCAGGAGAGCCAAAGAGAGTCTCATTTATGCCAGCTCAACTTCCCA	1464
Db	1546	CAAGCCCGAGAAATCCAGGAGAGCCAAAGAGAGTCTCATTTATGCCAGCTCAACTTCCCA	1605
QY	1465	GGCTGTACACCCAGGCGCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATTCAGAA	1524
Db	1606	GGCTGTACACCCAGGCGCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATTCAGAA	1665
QY	1525	GTCAAGTTCCAA	1536
Db	1666	GTCAAGTTCCAA	1677

RESULT 6

RESULTS 6
US-09-978-189-258

US-09-578-189-258
; Sequence 258, Application US/09978189

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/ Publication No. US20030004102A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
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/ APPLICANT: Hillan, Kenneth J.
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/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James,
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ TITLE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: P2630PIC7
/ CURRENT APPLICATION NUMBER: US/09/978,189
/ CURRENT FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: 09/918585
/ PRIOR FILING DATE: 2001-07-30
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PRIOR APPLICATION NUMBER: 60/085697

Query Match 70.2%; Score 1078.8; DB 10; Length 2764;

Best Local Similarity 81.4%; Pred.No. 0;

Matches 1329; Conservative 0; Mismatches 207; Indels 96; Gaps 3;

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QY 61 TTCTGGATACGAGTGCAGGAGTCAAGTGCATGTCGCGAGGCGCTGTCATCTCTGTGCC 120
DB 106 TTCTGGATACGAGTGCAGGAGTCAAGTGCATGTCGCGAGGCGCTGTCATCTCTGTGCC 165
QY 121 TGCTCTTCTCTCTACCCCGACAGACTGGACAGGCTTACCCAGCTTATGGCTACTGG 180
DB 166 TGCTCTTCTCTCTACCCCGACAGACTGGACAGGCTTACCCAGCTTATGGCTACTGG 225
QY 181 TTCAAGCAGTGAAGTGCAGCAACCAAGGGTCTCTGTGCGCCACAAACCAACCAAGAGTCGA 240
DB 226 TTCAAGCAGTGAAGTGCAGCAACCAAGGGTCTCTGTGCGCCACAAACCAACCAAGAGTCGA 285

241 GAGGTGGAATGAGACCGCGGGCCGATTTCCAGCTCAGTGGGATCCCGCCAAAGGGGAC 300
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Qy
301 TGCTCTCTGGTATCAGAGACGCGGAGATGCGAGATGAGTCAAGTACTTCTTTGGGGTG 360
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346 TGCTCTCTGGTATCAGAGACGCGGAGATGCGAGATGAGTCAAGTACTTCTTTGGGGTG 405
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361 GAGAGAGGAGCTATGTGAGATATAATTTATGAAAGATGGGTCTTTTCTAAAGTAACA 420
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406 GAGAGAGGAGCTATGTGAGATATAATTTATGAAAGATGGGTCTTTTCTAAAGTAACA 465
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466 GTGCTCAGCTTACGCGCCAGACCCAGGACCAACACCGACTCAGCTGCCATGTGGAC 525
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460 -----CTGGAGCGCGGACACCGCGGTGACGTT 485
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526 TTCTCAGAAAGGCTGTGAGCGCACAGAGGACCGTCCGACTCGTGTGGCTATGCCGCC 585
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486 CATCTGTGTGTTAACTGGGCCCTTTGAGGAATGTCCACCCCTCTTTCTCTGAGCGGG 545
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586 AGAGACCTTGTATCAGACTTTTCACTGTGACACACCGCAGCCCTGAGGCCCGACGCCAG 645
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546 GGCTGCTCTCTCTCCCAAGGAAACCAACGAGCTCCCACTTCTCAGTGTCTCAGCTT 605
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646 GGAATGTCCATACCTGGAAGCCCAAAAGGCGAGTTCCTGGGCTCTCTGTGTCTGT 705
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606 CAGCCCGACCCCGAGACCAAC-----GACACCGACTCAC 641
Db
706 GACAGCCAGCCCGCTGCCACTGAGCTGGGTCTTCAGAACAGAGTCTCTCTCTGCTCC 765
Qy
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Qy
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826 GGGCGCTACACTCGCGAGCGGAGAACAGGCTTGGCTCCAGCAGCGAGCCCTGGACCTC 885
Qy
753 -----AGATCCTCCAGAGACCTCAGAGTATGTTTCCCAAGCAACAGGACAGTC 804
Db
886 TCTGTGAGTATCTCTCAGAGAACCTTGAAGTATGTTTCCCAAGCAACAGGACAGTC 945
Qy
805 CTGGAACCTTGGGACGCGACGCTCTCTCCAGTACTGGAGGGCCAAAGCCCTGTCCCTG 864
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1126 CAGAGGAGAGTTACCTGCGACGCTGCGACACCACTGGGCTCCAGACAGTCTCTCTC 1185
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1045 AGCTCTCGTGTACTATAGAGGAGTCTATCTCAAGCGCATCTCCCAATGGAGGTTT 1104
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Db
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Qy 1225 ATCTGGATTACATCAATGTGTCTCCGACGCTGGCCCTGGCTCAGAACGGAATCAG 1284
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RESULT 7
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; Sequence 258, Application US/0978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James,
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 258
; LENGTH: 2764
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-608A-258

Query Match 70.2%; Score 1078.8; DB 10; Length 2764;
Best Local Similarity 81.4%; Pred. No. 0;
Matches 1329; Conservative 0; Mismatches 207; Indels 96; Gaps 3;

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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavind, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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, PRIOR APPLICATION NUMBER: 60/085704
, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/085697

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Query March	70.2%;	Score 1078.8;	DB 10;	Length 2764;
Best Local Similarity	8.4%;	Field No. 0;		
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Qy	1	ATGCTACTGCCACCTGCTCTCTCTCGCTGCTGCGCGGGTCCCAGGCTATGGATGGGAGA	60	
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Qy	61	TTCTGGATACGAGTGCAGGAGTCACTGATGATGTTGCCGAGGGCTTGTCATCTCTGTGCC	120	
Db	106	TTCTGGATACGAGTGCAGGAGTCACTGATGATGTTGCCGAGGGCTTGTCATCTCTGTGCC	165	
Qy	121	TGCTCTTTCTCCTACCCCGCAGACACGAGGCTCTACCCAGGCTATGGCTACTG	180	
Db	166	TGCTCTTTCTCCTACCCCGCAGACACGAGGCTCTACCCAGGCTATGGCTACTG	225	
Qy	181	TTCAAAGCAGTGACTGAGACAAACCAAGGCTGCTCTGTGGCCACAAACCCACAGAGTCGA	240	
Db	226	TTCAAAGCAGTGACTGAGACAAACCAAGGCTGCTCTGTGGCCACAAACCCACAGAGTCGA	285	
Qy	241	GAGGTGGAATAGACACCGGGGCCGATTCAGCTCACTGGGGATCCGCCCAAGGGGAAC	300	
Db	286	GAGGTGGAATAGACACCGGGGCCGATTCAGCTCACTGGGGATCCGCCCAAGGGGAAC	345	
Qy	301	TGCTCTTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTCTTTTCGGGTG	360	
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Qy	361	GAGAGAGGAAGCTATGTGAGATATAATTTCTATGAACGATGGGTTCTTCTAAAAGTAAACA	420	
Db	406	GAGAGAGGAAGCTATGTGAGATATAATTTCTATGAACGATGGGTTCTTCTAAAAGTAAACA	465	

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Db	466	GTGCTCAGCTTCACGGCCCGACACCCACAGGACCAACAACCGACTCCTGCCATGTGAC	525
Qy	460	-----CTGGAGCCGGGACAGCGGTGACGGT	485
Db	526	TTCTCCAGAAAGGGTGTGAGCGCACAGAGACCGTCCGACTCCGTGTGGCTATGCCCC	585
Qy	486	CATCTGTGTGTTTAACTGGGCCCTTTGAGGAATGTCCACCCCTTCTTTCTCTCTGGACGGG	545
Db	586	AGAGACCTTGTATTATCAGCAATTTACAGTGAACAACCGCAGCCTCGAGCCCCACGCCACG	645
Qy	546	GGCTGCCCTCTCTCCCAAGGAACCAACCAACGACTCCCATCTTCTCAGTGTCTCAGCTT	605
Db	646	GGAAATGTCCATACCTGTGAAGCCCAAAAGGCCAGTTCTCTGGGCTCTCTGTGCTGCT	705
Qy	606	CAGCCCGACACCCAGGACCAAC-----GACACCGACCTCAC	641
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Qy	702	GGCTATGCCCCCGACAGACCTTGTATTACGATTTTACGTGAACAACGCG-----	752
Db	826	GGGCGTACACTTCCGAGCGGGAACAGGCTTGGCTCCGACGACGAGCCCTGGAACCTC	885
Qy	753	-----AGATCTCCAGAAACCTCAGAGTATGATGTTTCCCAAGCAAAACAGACAGTC	804
Db	886	TCGTGTGAGTATCTCTCAGAGAACCTCAGAGTATGATGTTTCCCAAGCAAAACAGACAGTC	945
Qy	805	CTGAAAACCTTGGAAACGGCAGCTCTCTCCCACTACTGGAGGCCCCAAAGCCTGTGCTG	864
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Qy	925	CTGAGCCCCCTCCAGACCTCAGACCCCGGGTCTCTGAGCTGTGCTCGGTTTCAAGTGGAG	984
Db	1066	CTGAGCCCCCTCCAGACCTCAGACCCCGGGTCTCTGAGCTGTGCTCGGTTTCAAGTGGAG	1125
Qy	985	CACGAAGGAGTTTCACTCCACGCTCGGACCCACTGGGCTCCAGACGTTCTCTCTC	1044
Db	1126	CACGAAGGAGTTTCACTCCACGCTCGGACCCACTGGGCTCCAGACGTTCTCTCTC	1185
Qy	1045	AGCTCTCCGTGCACATAGAAGGAGTCTATCTCAACGGCATCTCCATGGAGCGTTT	1104
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Qy	1105	CTGGGAATCGGCATCAGCGTCTTCTTTTCTCTGCTGGCCCTGTATCATCATGAAGATT	1166
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Db	1426	AAAGCCCAACCAACAGTCTCTCGGACCCCTCTCCACAGTGTCTCCCTCCCGCAAGTCA	1485
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RESULT 10

US-09-978-403A-258
Sequence 258, Application US/09978403A
Publication No. US20030050240A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630P1C17
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
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PRIOR APPLICATION NUMBER: 60/081838
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PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797


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; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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Best Local Similarity 81.4%; Pred. No. 0;
Matches 1329; Conservative 0; Mismatches 207; Indels 96; Gaps 3;

1	ATGCTACTGCCACTGCTGCTGCTCTGCTGCTGCGGGTCCACAGCTATGATGGGAGA	60
46	ATGCTACTGCCACTGCTGCTGCTCTGCTGCTGCGGGTCCACAGCTATGATGGGAGA	105
61	TTCTGGATAACAGTGCCAGGAGTCAGTGATGGTCCGGAGGGCTGTGCATCTCTCTGGCC	120
106	TTCTGGATAACAGTGCCAGGAGTCAGTGATGGTCCGGAGGGCTGTGCATCTCTCTGGCC	165
121	TGCTCTTTTCTCTACCCGCCACAGGACTGGACAGGGTCTACCCAGCTTATGGCTACTGG	180
166	TGCTCTTTTCTCTACCCGCCACAGGACTGGACAGGGTCTACCCAGCTTATGGCTACTGG	225
181	TTCAAGACAGTGACTGAGACAAACCAAGGGTCTCTGTGCCACAAACACACAGAGTCGA	240
226	TTCAAGACAGTGACTGAGACAAACCAAGGGTCTCTGTGCCACAAACACACAGAGTCGA	285
241	GAGGTGGAAATGAGCACCCCGGGCCGATTCCAGCTCACTGGGGATCCCGCCCAAGGGGAAC	300
286	GAGGTGGAAATGAGCACCCCGGGCCGATTCCAGCTCACTGGGGATCCCGCCCAAGGGGAAC	345
301	TGCTCTTTGTTGATCAGACAGCGCAGATGCAGATGAGTCAAGTACTTCTTTCCGGGTG	360
346	TGCTCTTTGTTGATCAGACAGCGCAGATGCAGATGAGTCAAGTACTTCTTTCCGGGTG	405
361	GAGAGGAAAGCTATGTGAGATATAATTTCAAGACGATGGGTTCCTTTCTAAAGTAACA	420
406	GAGAGGAAAGCTATGTGAGATATAATTTCAAGACGATGGGTTCCTTTCTAAAGTAACA	465
421	GCCCTGACTCAGAAGCCTGATGTCTACATCCCGAGACC-----	459
466	GTGCTTCAGCTTTCACGCCCCAGACCCAGGACCAACACCGAGCTCACCTGSCCATGTGGAC	525
460	-----CTGGAGCCCGGCGACCGCGTGACGGT	485
526	TTCTCCAGAAAGGTGTGAGGCACAGAGGACCGTCCGACTCCGTGTGGCTTATGCCCCC	585
486	CATCTGTGTGTTTAACCTGGGCTTTTGAGGAATGTCACCCCTTCTTTCTCTCGACGGG	545
586	AGAGACCTTGTTATCAGCATTTACGCTGACAAACGACCGACGCTGGAGCCCGACGCCAG	645
546	GGCTGCCCTCTCCTCCCAAGAACCAACCAAGACCTCCCACTTCTCAGTGCTCAGCTT	605
646	GAAATGTCCCATACCTGGAGGCCAAAAAGGCCAGTTCTCTGGGGTCTCTCTGTGCTGCT	705
606	CACGCCCCAGACCCACGAGCACAC-----GACACCGAGCTCAC	641

706 GACAGCCAGCCCTGCGCACTGAGCTGGTCTGCGAAGACAGAGTCTCTCTCTGTC 765
642 CTGCCATGTGGACTTCTCCAGAAAGGTGTGAGGCGACAGAGACCGTCCGATCCGTTGT 701
766 CATCCCTGGGGCCCTAGACCCCTGGGCTGGAGTGCCTGGGTGAAGGCTGGGGATTCA 825
702 GGCCTATGCCCCCAGAGACCTTGTATACAGATTTCAGTGAACACAGCC----- 752
826 GGGCGCTACCTCCGAGCGGAGACAGGCTGGCTCCAGCAGCGAGCCCTGGACCTC 885
753 -----AGATCTCCAGAGAACCTGAGAGTATGTTTCCAGCAACACAGAGCAGTC 804
886 TCTGTGAGTATCTCCAGAGAACCTGAGAGTATGTTTCCAGCAACACAGAGCAGTC 945
805 CTGGAACCTTGGAAACGCGACGTCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCTG 864
946 CTGGAACCTTGGAAACGCGACGTCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCTG 1005
865 GTCTGTGTACACACAGCAGCCCTCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAGGTT 924
1006 GTCTGTGTACACACAGCAGCCCTCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAGGTT 1065
925 CTGAGCCCTTCCAGGCTCTAGACCCCGGGTCTCTGGAGTGGCTCGGTTCAAGTGGAG 984
1066 CTGAGCCCTTCCAGGCTCTAGACCCCGGGTCTCTGGAGTGGCTCGGTTCAAGTGGAG 1125
985 CACGAAGAGAGTTCACTGCTCGACCTCGGACCCAGCTGGGCTCCAGCAGCTCTCTCTC 1044
1126 CACGAAGAGAGTTCACTGCTCGACCTCGGACCCAGCTGGGCTCCAGCAGCTCTCTCTC 1185
1045 AGCTCTCTCGTGCATATAAGAGGACTCATCTCAACGGCATCTTCCATGAGGCGTTT 1104
1186 AGCTCTCTCGTGCATATAAGAGGACTCATCTCAACGGCATCTTCCATGAGGCGTTT 1245
1105 CTGGGATCGGCTACAGGCTCTTCTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1164
1246 CTGGGATCGGCTACAGGCTCTTCTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1305
1165 CTACGAGAGAGCGGACTCAGACAGAAACCCCGAGGCTTCTCCGCGCAGACAGC 1224
1306 CTACGAGAGAGCGGACTCAGACAGAAACCCCGAGGCTTCTCCGCGCAGACAGC 1365
1225 ATCTGATATCATATGTTGGTCCGACGGCTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCT 1284
1366 ATCTGATATCATATGTTGGTCCGACGGCTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1425
1285 AAAGCCACACAAACAGTCTCGGACCCCTCTTCCAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1344
1426 AAAGCCACACAAACAGTCTCGGACCCCTCTTCCAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1485
1345 AAGAGAACAGAAAGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1404
1486 AAGAGAACAGAAAGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1545
1405 CAAGCCACAGAAATCCAGGAGCGAGAGAGTCCATTATCCAGCTCACTTCCCA 1464
1546 CAAGCCACAGAAATCCAGGAGCGAGAGAGTCCATTATCCAGCTCACTTCCCA 1605
1465 GGCTCAGACCCAGGCTGAGGCGCGGATGCCCAAGGGCCACCCAGGCGGATATGAGAA 1524
1606 GGCTCAGACCCAGGCTGAGGCGCGGATGCCCAAGGGCCACCCAGGCGGATATGAGAA 1665
1525 GTCAGTTCCAA 1536
1666 GTCAGTTCCAA 1677

RESULT 12

US-09-937-636-1

Sequence 258, Application US/09999833A

Publication No. US20030054405A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PLC65
CURRENT APPLICATION NUMBER: US/09/999,833A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
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6	PRIOR FILING DATE: 1998-04-29
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9	PRIOR APPLICATION NUMBER: 60/083742
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23	PRIOR APPLICATION NUMBER: 60/084598
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25	PRIOR APPLICATION NUMBER: 60/084600
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33	PRIOR APPLICATION NUMBER: 60/085338
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46	PRIOR FILING DATE: 1998-05-15
47	PRIOR APPLICATION NUMBER: 60/085573
48	PRIOR FILING DATE: 1998-05-15
49	PRIOR APPLICATION NUMBER: 60/085704
50	PRIOR FILING DATE: 1998-05-15
51	PRIOR APPLICATION NUMBER: 60/085697

Query Match	81.2%	Seq. ID	82.2%
Best Local Similarity	81.4%	Pred. No.	0
Matches 1329; Conservative	0	Mismatches	207
Matches 1329; Conservative	0	Indels	96
Matches 1329; Conservative	0	Gaps	3

1	ATGCTACTGCCACTGCTGCTCTCTCTCTCTCTGGGGGGTCCAGAGCTATGGATGGGAGA	60
46	ATGCTACTGCCACTGCTGCTCTCTCTCTCTGGGGGGTCCAGAGCTATGGATGGGAGA	105
61	TTCTGGATACAGTGCAGGAGTCAGTCATGGTCCCGAGAGGCGCTGTGCATCTCTGTGCCC	120
106	TTCTGGATACAGTGCAGGAGTCAGTCATGGTCCCGAGAGGCGCTGTGCATCTCTGTGCCC	165
121	TGCTCTTTTCTCTTACCCCGCAGAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGG	180
166	TGCTCTTTTCTCTTACCCCGCAGAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGG	225
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226	TTCAAAGCAGTGCATGAGACAAACCAAGGGTGCTCTGTGGCCACAAACCAACCAAGTCCGA	285
241	GAGGTGGAAATGAGCACCCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAAGGGGAAC	300

286	DB		GAGGTGGAAATGAGCACCGGGGCGGATTCAGACTCACTGGGGATCCCGCAAGGGGAAC	345
301	QY		TGCTCTTTGGTGATCAGAGACGGCAGATCAGAGATGAGTCACAGTACTTCTTTCCGGGTG	360
346	DB		TGCTCTTTGGTGATCAGAGACGGCAGATGAGATGAGTCAAGTACTTCTTTCCGGGTG	405
361	QY		GAGAGAGAACTATGTGAGATAATAATTTATGAACGATGGTTCTTTCTAAAAGTAACA	420
406	DB		GAGAGAGAACTATGTGACATATAATTTATGAACGATGGTTCTTTCTAAAAGTAACA	465
421	QY		GCCCTGACTCAGNAGCCTGATGTCTACATCCCGAGACC-----	459
466	DB		GTGCTCAGCTTCACGCCCGACGCCAGGACCAACACCGACTCACTCGCATGTGGAC	525
460	QY		-----CTGGAGCCCGGCGACCGGTGACGGT	485
526	DB		TTCTCCAGAAAGCGTGTAGCGCACAGAGGACCGTCCGACTCGGTGGCTATGCCCC	585
486	QY		CATCTGTGTGTTAACTGGGCCCTTTCAGGATGTCAACCCCTCTTTCTCTGTGACGG	545
586	DB		AGAGACCTTGTATCAGCAATTCAGGTGACACACGCCAGCCCTGGAGCCCGACGCCCGAC	645
546	QY		GGCTGCCCTCTCTCCCAAGGACCAAAACACAGACTCCCACTTCTCAGTGTCTCAGCTT	605
646	DB		GGAAATGTCCCATACCTTGAAGCCCAAAAGGCCAGTCTCTGGGCTCTCTGTGTCTGT	705
606	QY		CACGCCCAGACCCAGAGCAC-----GACACCGACCTCAC	641
706	DB		GACAGCCAGCCCCCTGCCACACTAGCTGGTCTCTCAGAACAGAGATCTCTCTCTGCTCC	765
642	QY		CTGCCATGTGACTTCTCCAGAAAGGTTGTGAGCGCACAGAGGACCGTCCGACTCCGTGT	701
766	DB		CATCTCTGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGCTGGGGATTCAC	825
702	QY		GGCTATGCCCCCAGAGACCTTGTATCAGCAATTCAGGTGACAAACAGCC-----	752
826	DB		GGCGCTACACTCCGAGCGGAGAACAGGCTGGCTCCACAGCAGGACCCCTGGACCTC	885
753	QY		-----AGATCTCCAGAGAACCTGAGAGTATGTTTCCAGAGCAACAGCAGACGTC	804
886	DB		TCTGTGAGTATCTCCAGAGAACCTGAGAGTATGTTTCCAGAGCAACAGCAGACGTC	945
805	QY		CTGGAACCTTGGAAACGCAAGTCTCTCCAGTACTGGAGGGCCAAAGCCTCTGGCTG	864
946	DB		CTGGAACCTTGGGAACGCAAGTCTCTCCAGTACTGGAGGGCCAAAGCCTCTGGCTG	1005
865	QY		GTCTGTGTACACACAGCAGCCCCCAGCCAGGCTGAGTGTGACCCAGAGGGGACAGTT	924
1006	DB		GTCTGTGTACACACAGCAGCCCCCAGCCAGGCTGAGCTGACCCAGAGGGGACAGTT	1065
925	QY		CTGAGCCCTCCAGCCCTCAGACCCCGGGTCTCTGGAGTGCCTCGGGTTCAGATCGAG	984
1066	DB		CTGAGCCCTCCAGCCCTCAGACCCCGGGTCTCTGGAGTGCCTCGGGTTCAGATCGAG	1125
985	QY		CACGAAGAGAGTTCACCTGCCAAGTCCGACCAACTGGGTCCAGCAGTCTCTCTC	1044
1126	DB		CACGAAGAGAGTTCACCTGCCAAGTCCGACCAACTGGGTCCAGCAGTCTCTCTC	1185
1045	QY		AGCTCTCCGTGCACCTATAGAAGGACATCATCAACGGCATTTCTCAATGGAGCGTTT	1104
1186	DB		AGCTCTCCGTGCACCTATAGAAGGACATCATCAACGGCATTTCTCAACGGAGCGTTT	1245
1105	QY		CTGGAAATCGGCATCAGCGCTCTCTTTTCTCTGCCCTGGCCCTGATCATCAAGATT	1164
1246	DB		CTGGAAATCGGCATCAGCGCTCTCTTTTCTCTGCCCTGGCCCTGATCATCAAGATT	1305
1165	QY		CTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGCCAGGTTCTCCCGCAGACGACG	1224
1306	DB		CTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGCCAGGTTCTCCCGCAGACGACG	1365
1225	QY		ATCTCGATTACATCAATGTGTCCCGACGGGTGCCCGCTTGCTCAGAGCGGAATCAG	1284

Db	1366	ATCCTGGATTACATCAATGTGTGCCGACGGCTGGCCCCCTCGCTCAGAAAGCGGAATCAG	1422
Qy	1285	AAAGCCACACCAAAACAGTCTCTGGACCCCTCTTTCCACACAGGTGCTCCCTCCCGCAGAAATCA	1344
Db	1426	AAAGCCACACCAAAACAGTCTCTGGACCCCTCTTCCACACAGGTGCTCCCTCCCGCAGAAATCA	1485
Qy	1345	AGAAGAAACAGAAAAAGCAGTATCAGTTGCCAGTTTCCGAGAACCCAAATCATCCACT	1404
Db	1486	AGAAGAAACAGAAAAAGCAGTATCAGTTGCCAGTTTCCGAGAACCCAAATCATCCACT	1545
Qy	1405	CAAGCCCCCAGATCCCCAGGAGAGCCCAAGAGGAGCTCCATTATGSCCAGGCTCAACTTTCCCA	1464
Db	1546	CAAGCCCCCAGATCCCCAGGAGAGCCCAAGAGGAGCTCCATTATGSCCAGGCTCAACTTTCCCA	1605
Qy	1465	GGCGTCAGACCCACAGGCGCTGAGGCCCGGATGCCCAAGGGCAACCCAGGCGGATATGCGAGAA	1524
Db	1606	GGCGTCAGACCCACAGGCGCTGAGGCCCGGATGCCCAAGGGCAACCCAGGCGGATATGCGAGAA	1665
Qy	1525	GTCAAGTTCCAA	1536
Db	1666	GTCAAGTTCCAA	1677

RESULT 13

US-09-981-915A-258

Sequence 258, Application US/09981915A

Publication No. US20030054986A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secured and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2630PIC12

CURRENT APPLICATION NUMBER: US/09/981,915A

CURRENT FILING DATE: 2001-10-16

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

PRIOR APPLICATION NUMBER: 60/082566	PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569	PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796	PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336	PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322	PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083399	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558	PRIOR FILING DATE: 1998-04-30
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PRIOR APPLICATION NUMBER: 60/085323	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580	PRIOR FILING DATE: 1998-05-15

APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC14
CURRENT APPLICATION NUMBER: US/09/978,824
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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Db 1666 GTCAAGTCCAA 1677

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; GENERAL INFORMATION:
; APPLICANT: Askenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mackey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
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Qy	606	CAGCCCCAGACCCGAGGACCAC-----GACACCGACCTCAC	641
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 07:56:39 ; Search time 7194.25 Seconds
(without alignments)
7780.028 Million cell updates/sec

Title: US-09-937-636-1

Perfect score: 1536

Sequence: 1 atgctactccactgctgtct.....atgcagaagtcgaattccaa 1536

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2: *
3: gb_hic: *
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8: gb_gssi: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	537.2	35.0	1099	4	BM544297 AGENCOURT
3	478	31.1	667	6	CB554607 MMSP0040
4	448.8	29.2	514	5	EX470328 DXF29779N
5	413	26.9	1464	4	BM544269 AGENCOURT
6	372.8	24.3	1745	4	BM906520 AGENCOURT
7	338	22.0	2017	3	AK042488 Mus muscu
8	324.8	21.1	1313	3	CR614233 full-leng
9	324.8	21.1	1821	3	CR600025 full-leng
10	320.6	20.9	871	4	B1518708 603082076
11	320.6	20.9	1714	3	BC030222 Homo sapi
12	307.2	20.0	505	5	EX283650 BX283650
13	307.2	19.6	936	2	BF663289 602144414
14	301.6	20.0	3939	3	AK036698 Mus muscu
15	296.8	19.3	1121	4	BM564074 AGENCOURT
16	294.4	19.2	730	7	CN389197 170004245
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18	287	18.7	2220	3	BC035688 Homo sapi
19	286.4	18.6	1071	4	BM920861 AGENCOURT
20	285	18.6	876	5	BQ711946 AGENCOURT
21	280	18.2	995	4	BM922784 AGENCOURT
22	278.4	18.1	825	7	CR629578
23	276.6	18.0	1060	4	BM925147 AGENCOURT
24	276	18.0	1012	4	BM922958 AGENCOURT

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28	265.8	17.3	1028	5	BX399458	BX399458
29	265.8	17.3	1522	3	CR592075	CR592075
30	253.8	16.5	857	5	BQ883649	AGENCOURT
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35	245	16.0	997	4	BM9221873	AGENCOURT
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37	241.6	15.7	815	5	BP436349	BP436349
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ALIGNMENTS

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DEFINITION BX345667 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSOD1025YC24 5-PRIME, mRNA sequence.
ACCESSION BX345667
VERSION BX345667 GI:46290734
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1011)
AUTHORS Li.W.B., Gruber.C., Jesse.J. and Polayes.D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 5, 2003 this sequence version replaced gi:30373021.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of invitrogen. This sequence belongs to sequence cluster
9384.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CSOA1025BB12QPl&c=9384.r.

FEATURES

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sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 36.8%; Score 565.4; DB 5; Length 1011;
Best Local Similarity 77.7%; Pred. No. 2.1e-141;
Matches 750; Conservative 4; Mismatches 160; Indels 51; Gaps 4;


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QY 482 CGTCTCTGTGTGTTAACTGGGCTTTGAGAAATGTCAACCCCTTCTTTCTCTCTGA 541
DB 526 CGTCTCTGTGTGTTAACTGGGCTTTCAAGAAATGTCAAGCCCTTCTTTCTCTCTGA 585
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DB 646 GTTTCAGCCAGCAGCCAGGACCAAGACCAAGCAGCCTCCCACTTCTCAGTCTCA 705
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DB 706 GAAAGGTTGAGCGACAGGACCGTCCCGACTCCGTTGGCCT 751

RESULT 3
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DEFINITION WMSP0040_D05 MMSP Macaca mulatta cDNA, mRNA sequence.
ACCESSION CB554607
VERSION CB554607.1 GI:31303802
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 667)
AUTHORS Katze, M.G., Bungartner, R., Korth, M., Feldman, R., Amjadi, M. and
Holzman, T.
TITLE Expressed sequence tags from Rhesus macaque spleen
JOURNAL Unpublished (2002)
COMMENT Contact: Holzman T
Katze Lab
University of Washington
Box 358070, Seattle, WA 98195-8070, USA
Tel: 206 732 6156
Fax: 206 732 6055
Email: ted@locke.hs.washington.edu
Similar to GenBank entry AF311905 AF311905 Homo sapiens sialic
acid-binding Ig-like lectin 10 (SIGLEC10) mRNA, complete cds.
8/2001
Plate: WMSP0040 row: D column: 05.
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1..667
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/cell_type="monocytes"
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/notes="Organ: spleen"

Query Match 31.1%; Score 478; DB 6; Length 667;
Best Local Similarity 94.8%; Pred. No. 8.3e-118;
Matches 506; Conservative 0; Mismatches 25; Indels 3; Gaps 1;

QY 1006 CAGCTCGGACCCACCTGGGCTCCAGCAGCTCTCTCAGCCTCTCCGTGACCTATAAG 1065
DB 1 CAGCCTCAGACCCCGTGGTGGTCTCAGCAGCTCTCTCAGCCTCTCCGTGACCTATAAG 60
QY 1066 AAGGACTCATCTCAACGGCATCTCCAAATGGAGCGTTTCTGGGAATCGGCATCAGCGCT 1125
DB 61 AAGGACTCATCTCAACGGCATCTCTCCAGGAGCGTTTCTGGGAATCGGCATCAGCGCT 120

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QY 1126 CTTCTTTTCTCTGCTGGCCCTGATCATCATGAAGATTTACCGAAGAGACGACTCAG 1185
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QY 1186 ACAGAAACCCGAGCCCGAGGTCTCCGGGACAGCAGATCTCGGATTAATCATCATGTG 1245
DB 181 GCAGATACCCCAAGGCCCGAGGTCTCCGGGACAGCAGATCTCGGATTAATCATCATGTG 240
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DB 241 GTCCCGAAGGCGGGCCCTGGCTCAGAAATCGGAATCAGAAAGCCACACCAAGCAGTCT 300
QY 1304 -CTCGAGCCCTCTTTCACAGGTGCTCTCCCTCCCGAGAAATCAAAAGAAACACGAAAAAG 1362
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QY 1363 CAGTATCAGTTGCCAGTTTCCAGAACCCAAATCATCTCAAGCCCGCAGATCCCGAG 1422
DB 361 CAGCATCAGTTGCCAGTTTCCAGAACCCAAATCATCTCAAGCCCGCAGATCCCGAG 420
QY 1423 GAGAGCCCAAGGAGGAGCTCCATTATGCCACGCTCACTTCCAGGCGTCAGACCCAGGCT 1482
DB 421 GAGAGCCCAAGGAGGAGCTCCATTATGCCACGCTCACTTCCAGGCGTCAGACCCAGGCT 480
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DB 481 GAGGCCCGGATCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 534

RESULT 4
LOCUS BX470328 514 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp779N169_r1 779 (synonym: hnccl) Homo sapiens cDNA clone
ACCESSION BX470328
VERSION BX470328.1 GI:32023094
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 514)
AUTHORS Bloeker, H., Boecker, M., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
Fobo, G., Han, M. and Wiemann, S.
EST (Bioecker, H., Boecker, M., Mewes, H.W., Weil, B., Amid, C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No s1 sequence available.
This clone (DKFZp779N169) is available at the RZPD in Berlin.
Please contact the RZPD, Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
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/clone_lib="779 (synonym: hnccl)"
/notes="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIB"
ORIGIN

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AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs@mail.nih.gov
 Tissue Procurement: Invitrogen
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAM12364 row: 0 column: 15
 High quality sequence start: 64
 High quality sequence stop: 538.
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 /db_xref="taxon:9606"
 /clone="IMAGE:5590502"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_125"
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ORIGIN

Query Match 24.3%; Score 372.8; DB 4; Length 1745;
 Best Local Similarity 82.3%; Pred. No. 3.2e-59;
 Matches 428; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

Qy 2 TGTACTGCCACTGCTGCTCTCTCTGCTGCTGGCGGGTCCAGGCTATGGATGGAGAT 61
 Db 107 TGTCTGCTGCCCTGCTGCTGCCGCTGCTGGGGCGGGTCCCTGAACAGGATCCAGAT 166

Qy 62 TCTGGATACAGTGCAGGAGTCACTGATGTCGCGGAGGCTGTGCTCATCTCTGTCCT 121
 Db 167 ACAGTCTTCAAGTGCAGAGCGAGTGCCTGTCGCGGAGGCTGTGCTCATCTGCTCT 226

Qy 122 GCTCTTTCTCTACCCCGACAGGACTGGACAGGCTTACCCAGCTTATGGCTACTGCT 181
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Qy 182 TCAAGCAGTCACTGACACCAACAGGCTGCTCTGTGGCCACCAACACGAGTCGAG 241
 Db 287 TCAAGGACGCGACGACCCAAAGACGCGTCTCTGTGGCCACTAAACACGAGTCGAG 346

Qy 242 AGTGGAATAGCACCCGCGCGGATCTCCAGTCTACTGGGATCCGCAAGGGAACT 301
 Db 347 AGTGGAATAGCACCCGCGCGGATCTCCAGTCTACTGGGATCCGCAAGGGAGCT 406

Qy 302 GTCCTTGTGTGATCAGAGACGCGCAGATGAGTCACTGATGATGATGATGATGATG 361
 Db 407 GTCCTTGTGTGATCAGAGACGCGCAGAGGAGGATGAGGATGATGATGATGATGATG 466

Qy 362 AGAGGGAAGCTATGTGAGATATAATTTCTATGACGATGGTCTTTCTAAAGTAACAG 421
 Db 467 AGAGGGAAGCTATGTGAGATATAATTTCTATGACGATGGTCTTTCTAAAGTAACAG 526

Qy 422 CCTGACTCAGAGCCTGATGCTTACATCCCGAGACCTTGGAGCCCGGCGAGCGGTGA 481
 Db 527 CCTGACTCAGAGCCTGATGCTTACATCCCGAGACCTTGGAGCCCGGCGAGCGGTGA 586

Qy 482 CGTCACTCTGTGTTTAACTGGCCCTTTGAGGAATGTC 521
 Db 587 CGTCACTCTGTGTTTAACTGGCCCTTTTAAAGAAATGTC 626

RESULT 7

AK042488 2017 bp mRNA linear HTC 03-APR-2004
 Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630096C01 product:weakly similar to SIALIC
DEFINITION ACID-BINDING LECTIN [Homo sapiens], full insert sequence.
 AK042488.1 GI:26335142
ACCESSION AK042488
VERSION AK042488.1
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Carninci, P., and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
 PUBMED 10349636

2
REFERENCE Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 PUBMED 11042159

3
REFERENCE Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 PUBMED 11076861

4
REFERENCE The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 403, 685-690 (2001)

5
REFERENCE The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 2017)

6
REFERENCE Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel:81-45-503-9222,

TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel:81-45-503-9222,

Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC Building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>.

FEATURES

source
1. 2017
/location/Qualifiers
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147..>2015
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882 -----AATGTATCAGTCTCCAGCTTGCATCAGAAATCTTTCACATCTGGAAGTTCAG 932
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ORIGIN

Query Match 22.0%; Score 338; DB 3; Length 2017;
Best Local Similarity 61.8%; Pred. No. 8,6e-80;
Matches 658; Conservative 0; Mismatches 340; Indels 66; Gaps 5;
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273 TCTTCT 332
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304 TCTTGTGATCAGAGCGGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 363
453 TCTTGTGATCAAGATGTTTCAAGTGGGAGACTCAACAAACTATTCTTCCGGATGGAG 512

RESULT 8
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DEFINITION
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ACCESSION
CR614233
VERSION
CR614233.1 GI:50495040
KEYWORDS
HTC; CNSL; cDNA.
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1313)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : liang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Paradise Avenue
Genoscope.
2 (bases 1 to 1313)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqlife@genoscope.cns.fr)

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VERSION BI518708.1 GI:15343500
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 871)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM1530 row: 9 column: 20
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and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."
ORIGIN
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Best Local Similarity 80.7%; Pred. No. 3.5e-75;
Matches 388; Conservative 0; Mismatches 89; Indels 4; Gaps 1;
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Db 232 TCAAGAGTGCAGTGCAGCAACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 291

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
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www.rzpd.de

This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
PCW-M13u. Primer sequence: CGTGTAAACGACGGCGGT.

FEATURES

Location/Qualifiers
1..505
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4297851"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 20.0%; Score 307.2; DB 5; Length 505;
Best Local Similarity 99.0%; Pred. No. 1.3e-71;
Matches 309; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 750 GCCAGATCTCCAGAGAACCTGAGAGTGTGTTCCCAAGCAAAACAGGACAGCTCTGGA 809
Db 6 GCAGTATCTCCAGAGAACCTGAGAGTGTGTTCCCAAGCAAAACAGGACAGCTCTGGA 65
QY 810 AACCTTGGGNAACGGACAGTCTCTCCAGTACTGAGGGCCAAAGCTGTGCTGTCTG 869
Db 66 AACCTTGGGNAACGGACAGTCTCTCCAGTACTGAGGGCCAAAGCTGTGCTGTCTG 125
QY 870 TGTACACACAGACAGCCCGCCAGCGCTGAGCTGAGTCCAGCCAGAGGGACAGTCTGAG 929
Db 126 TGTACACACAGACAGCCCGCCAGCGCTGAGCTGAGTCCAGCCAGAGGGACAGTCTGAG 185
QY 930 CCCTCCAGCCCTCAGACCCCGGGTCTTGGAGTGTGCTCGGGTCAAGTGGAGCAGCA 989
Db 186 CCCTCCAGCCCTCAGACCCCGGGTCTTGGAGTGTGCTCGGGTCAAGTGGAGCAGCA 245
QY 990 AGGAGAGTTACCTGCGACCTCGGCACCCACCTGGGCTCCAGACAGTCTCTCAGCCT 1049
Db 246 AGGAGAGTTACCTGCGACCTCGGCACCCACCTGGGCTCCAGACAGTCTCTCAGCCT 305
QY 1050 CTCGGTGCACCTA 1061
Db 306 CTCGGTGCACCTA 317

RESULT 13

BF663289
LOCUS 60214414F1 NIH_MGC_48 936 bp mRNA linear EST 21-DEC-2000
DEFINITION mRNA sequence.
ACCESSION BF663289
VERSION BF663289.1 GI:11937171
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 936)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MSC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1152 row: k column: 04
High quality sequence stop: 661.

FEATURES

Location/Qualifiers
1..936
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4297851"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 20.0%; Score 307.2; DB 2; Length 936;
Best Local Similarity 99.0%; Pred. No. 1.5e-71;
Matches 309; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 750 GCCAGATCTCCAGAGAACCTGAGAGTGTGTTCCCAAGCAAAACAGGACAGTCTGGA 809
Db 13 GCAGTATCTCCAGAGAACCTGAGAGTGTGTTCCCAAGCAAAACAGGACAGTCTGGA 72
QY 810 AACCTTGGGNAACGGACAGTCTCTCCAGTACTGAGGGCCAAAGCTGTGCTGTCTG 869
Db 73 AACCTTGGGNAACGGACAGTCTCTCCAGTACTGAGGGCCAAAGCTGTGCTGTCTG 132
QY 870 TGTACACACAGACAGCCCGCCAGCGCTGAGCTGAGTCCAGCCAGAGGGACAGTCTGAG 929
Db 133 TGTACACACAGACAGCCCGCCAGCGCTGAGCTGAGTCCAGCCAGAGGGACAGTCTGAG 192
QY 930 CCCTCCAGCCCTCAGACCCCGGGTCTTGGAGTGTGCTCGGGTCAAGTGGAGCAGCA 989
Db 193 CCCTCCAGCCCTCAGACCCCGGGTCTTGGAGTGTGCTCGGGTCAAGTGGAGCAGCA 252
QY 990 AGGAGAGTTACCTGCGACCTCGGCACCCACCTGGGCTCCAGACAGTCTCTCAGCCT 1049
Db 253 AGGAGAGTTACCTGCGACCTCGGCACCCACCTGGGCTCCAGACAGTCTCTCAGCCT 312
QY 1050 CTCGGTGCACCTA 1061
Db 313 CTCGGTGCACCTA 324

RESULT 14

AK036698
LOCUS AK036698
DEFINITION Mus musculus adult male bone cDNA, RIKEN full-length enriched
library, clone:9830164H23 product:weakly similar to SIALIC
ACID-BINDING LECTIN [Homo sapiens], full insert sequence.
ACCESSION AK036698
VERSION AK036698.1 GI:26331615
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Result No.	Score	Query Match	Length	DB ID	Description
1	1917	100.0	3099	6	BD011516 Sialoadhe
2	1917	100.0	3099	6	BD011517 Sialoadhe
3	1907.4	99.5	2295	6	BD261503 12 human
4	1905.8	99.4	2126	9	AY032685 Homo sapi
5	1868	97.4	2954	6	AX365517 Sequence
6	1733	90.4	2208	6	AX365530 Sequence
7	1733	90.4	3012	9	AF301007 Homo sapi
8	1733	90.4	3024	6	AX365542 Sequence
9	1729.8	90.2	2176	9	AF310233 Homo sapi
10	1497.4	78.1	2823	6	AX365518 Sequence
11	1337	69.7	2565	6	AX365516 Sequence
12	1333.8	69.6	2764	6	Q0767791 Sequence
13	1333.8	69.6	2764	6	AX376050 Sequence
14	1333.8	69.6	2764	9	AY358337 Homo sapi
15	1324.4	69.1	2076	6	Q0733422 Sequence
16	1277	66.6	2529	6	AX365544 Sequence
17	1217.8	63.5	1344	6	BD261712 12 human
18	1160	60.5	2052	6	AX365546 Sequence
19	1146.6	59.8	3124	9	AF311905 Homo sapi

DB	51	ATGCTACTGCCACTGCTGCTCTCGCTGCTGTGGCGGGTCCCAAGGCTATGATGGGAGA	111
QY	61	TTCTGGATACGAGTGCAGGAGTCAGTGATGTGTGCCGAGGGCCCTGTGCATCTCTGTGCC	120
DB	111	TTCTGGATACGAGTGCAGGAGTCAGTGATGTGTGCCGAGGGCCCTGTGTCATCTCTGTGCC	170
QY	121	TGCTCTTTTCTCCTACCCCGGACAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGG	180
DB	171	TGCTCTTTTCTCCTACCCCGGACAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGG	230
QY	181	TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCTGTGGCCACAACACCCAGAGTCGA	240
DB	231	TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCTGTGGCCACAACACCCAGAGTCGA	290
QY	241	GAGGTGMAATGAGACAACCCGGGGCGGATTCAGGTCACTGGGGATCCCGCCAAAGGGGAAC	300
DB	291	GAGGTGMAATGAGACAACCCGGGGCGGATTCAGGTCACTGGGGATCCCGCCAAAGGGGAAC	350
QY	301	TGCTCCTTGTGATCAGAGACGCGCAGATGCAGGATGATCACAAGTACTTCTTTCGGGTG	360
DB	351	TGCTCCTTGTGATCAGAGACGCGCGAGATGCAGGATGATCACAAGTACTTCTTTCGGGTG	410
QY	361	GAGAGGGAAGCTATGTGAGATATAATTTCAATGAACGATGGGTTCTTTCTAAAAAGTAACA	420
DB	411	GAGAGGGAAGCTATGTGAGATATAATTTCAATGAACGATGGGTTCTTTCTAAAAAGTAACA	470
QY	421	GTGCTCAGCTTCACGCGCCAGACCCAGGACCAACAACCGGACTCACTGCGCATGTGGAC	480
DB	471	GTGCTCAGCTTCACGCGCGACCCAGGACCAACAACCGGACTCACTGCGCATGTGGAC	530
QY	481	TTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCCGTGTGGCTATGCCCCC	540
DB	531	TTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCCGTGTGGCTATGCCCCC	590
QY	541	AGAGACCTTGTATCAGCATTTACGTGACAAACGCGCAGCCCTGAGAGCCCGCAGCCCCAG	600
DB	591	AGAGACCTTGTATCAGCATTTACGTGACAAACGCGCAGCCCTGAGAGCCCGCAGCCCCAG	650
QY	601	GGAAATGTCCTATACCTCGGAAGCCCAAAAGGCCAGTTCTCTGGGGCTCTCTGTGCTGCT	660
DB	651	GGAAATGTCCTATACCTCGGAAGCCCAAAAGGCCAGTTCTCTGGGGCTCTCTGTGCTGCT	710
QY	661	GACAGCAGCCCTTGCACACCTGAGCTGGGTCTGTGAGAACAGAGTCCTCTCTCTGCTCC	720
DB	711	GACAGCAGCCCTTGCACACCTGAGCTGGGTCTGTGAGAACAGAGTCCTCTCTCTGCTCC	770
QY	721	CATCCCTGGGGCCCTAGACCCCTGGGGCTGAGCTGCCGGGGTGAAGGCTGGGGGATTC	780
DB	771	CATCCCTGGGGCCCTAGACCCCTGGGGCTGAGCTGCCGGGGTGAAGGCTGGGGGATTC	830
QY	781	GGGCGCTACACTGCCAGCGGGAACAAGCCTTGGCTCCAGCAGCGAGCCCTGGACCTC	840
DB	831	GGGCGCTTACACTGCCAGCGGGAACAAGCCTTGGCTCCAGCAGCGAGCCCTGGACCTC	890
QY	841	TCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGAATGGTTTCCCAAGCAACACAGGACGTC	900
DB	891	TCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGAATGGTTTCCCAAGCAACACAGGACGTC	950
QY	901	CTGGAACACCTTGGGAACGGCAGCTCTCTCCCAAGTACTGGAGGGCCCAAGCCCTGTGCTG	960
DB	951	CTGGAACACCTTGGGAACGGCAGCTCTCTCCCAAGTACTGGAGGGCCCAAGCCCTGTGCTG	1010
QY	961	GTCTGTGTACACACAGCAGCCCGCCAGCGCTGAGCTGGAACCAAGAGGGGACAGGTT	1020
DB	1011	GTCTGTGTGTACACACAGCAGCCCGCCAGCGCTGAGCTGGAACCAAGAGGGGACAGGTT	1070
QY	1021	CTGAGCCCTTCCAGGCTTACAGCCCGGGGGTCTTGAGCTGCTCGGGTTCAAGTGGAG	1080
DB	1071	CTGAGCCCTTCCAGGCTTACAGCCCGGGGGTCTTGAGCTGCTCGGGTTCAAGTGGAG	1130
QY	1081	CACGAAGGAGGTTCTACTGCGACGCTGGGCAACCACTGGGGTCTCCAGACGCTCTCTCTC	1140
DB	1131	CACGAAGGAGGTTCTACTGCGACGCTGGGCAACCACTGGGGTCTCCAGACGCTCTCTCTC	1190

QY	1141	AGCCTCTCCGTGCACACTACTCCCGGAAGCTGCTGGGCCCTCTCTGCTCTCTGGGAGGCTGAG	1200
Db	1191	AGCCTCTCCGTGCACACTACTCCCGGAAGCTGCTGGGCCCTCTCTGCTCTCTGGGAGGCTGAG	1250
QY	1201	GGTCTGCACCTGCAGCTGCTCTCTCCAGGCAGCCCGGCCCTCTCTGTGGCTGTGGTGGCTT	1260
Db	1251	GGTCTGCACCTGCAGCTGCTCTCTCCAGGCAGCCCGGCCCTCTCTGTGGCTGTGGTGGCTT	1310
QY	1261	GGGAGAGAGCTGCTGGAGGGGAAACAGCAGCAGCAGACTCTCTTTCCGAGGTCAACCCGACCTCA	1320
Db	1311	GGGAGAGAGCTGCTGGAGGGGAAACAGCAGCAGCAGACTCTCTTTCCGAGGTCAACCCGACCTCA	1370
QY	1321	GCCGGGCCCTGGGCAACAGCTCTCTTGAGCCTCCATGGAGGGCTCAGCTCCGGCTTCAGG	1380
Db	1371	GCCGGGCCCTGGGCAACAGCTCTCTTGAGCCTCCATGGAGGGCTCAGCTCCGGCTTCAGG	1430
QY	1381	CTCCGCTGTGAGCGCTGGAGCGTCCATGGGGCCAGAGTGGATCCATCTCTGAGCTGCCA	1440
Db	1431	CTCCGCTGTGAGCGCTGGAGCGTCCATGGGGCCAGAGTGGATCCATCTCTGAGCTGCCA	1490
QY	1441	GATAAAGAGGACTCATCTCAACGGCATTTCTCAACGGAGCGGTTCTTGGGAATCGGCATC	1500
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QY	1621	AATGTGTCCTCCGAGCGTGGCCCTTGGCTCAGAGCGGGAATCAGAAAGCCACACCAAC	1680
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QY	1681	AGTCCTCGGACCCCTCTTCCACAGGTGCTCCCTCCCGAGATCAAAGAAAGAACAGAAA	1740
Db	1731	AGTCCTCGGACCCCTCTTCCACAGGTGCTCCCTCCCGAGATCAAAGAAAGAACAGAAA	1790
QY	1741	AACGATATCAGTGTGCCAGTTTCCAGAACCCAAATCATCACTCAAGCCCGAGATCC	1800
Db	1791	AACGATATCAGTGTGCCAGTTTCCAGAACCCAAATCATCACTCAAGCCCGAGATCC	1850
QY	1801	CAGGAGAGCCAGAGAGAGCTCCATTATGCCAGCTCACTTCCAGGGCTCAGAGCCAGG	1860
Db	1851	CAGGAGAGCCAGAGAGAGCTCCATTATGCCAGCTCACTTCCAGGGCTCAGAGCCAGG	1910
QY	1861	CCTGAGGCCCGATGCCAAGGGCACCCAGGCGGATTATGCAGAAAGTCAAGTTCCAA	1917
Db	1911	CCTGAGGCCCGATGCCAAGGGCACCCAGGCGGATTATGCAGAAAGTCAAGTTCCAA	1967
RESULT 2			
LOCUS	BD011517	3099 bp	DNA linear PAT 31-JAN-2002
DEFINITION	Sialoadhesin family 4 (SAF-4); cDNA.		
ACCESSION	BD011517		
VERSION	BD011517.1 GI:18639890		
KEYWORDS	JP 2001502359-A/2.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Kikly, K.K. and Miller, C.L.E.		
JOURNAL	Sialoadhesin family 4 (SAF-4) cDNA		
COMMENT	Patent: JP 2001502359-A 2 20-FEB-2001;		
	SMITHKLINE BEECHAM CORP		
	OS Homo sapiens (human)		
	PN JP 2001502359-A/2		
	PD 20-FEB-2001		

PF	27-MAY-1998 JP	1999500864
PI	27-MAY-1997 US	60/047572
PR	KRISTINE KAY KIKLY, CONNIE LYNN ERICKSON MILLER PC	
A51K38/00,A61K39/395,A61K48/00,C07H21/04,C07K14/435,C07K14/705,PC	C07K16/00,	
PC	C07K16/18,C07K16/28,C12N15/01,C12N15/11,C12N15/12,C12N15/63 CC	

FH	Key	Location/Qualifiers
FT	source	1..3099
FI	/organism='Homo sapiens (human)'	.
FEATURES	Location/Qualifiers	
source	1..3099	
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ORIGIN	
Query Match	100.0%; Score 1917; DB 6; Length 3099;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1917; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	TTCTGGATACG	TGCAGGAGTCAGTGTCGCGGAGGSCCTGTGCATCTCTGTGCC	120
Db	111	TTCTGGATACG	TGCAGGAGTCAGTGTCGCGGAGGSCCTGTGCATCTCTGTGCC	170
Qy	121	TGCTCTTTCT	CCTACCCCAGACAGCTGCAGGGTCTACCCAGCTTATGGCTACTGG	180
Db	171	TGCTCTTTCT	CCTACCCCAGACAGCTGCAGGGTCTACCCAGCTTATGGCTACTGG	230
Qy	181	TTCAAACGACTG	ACTGAGACAACAAGGTGCTCTCTGGCCCAAAACCACCAAGAGTCGA	240
Db	231	TTCAAACGACTG	ACTGAGACAACAAGGTGCTCTCTGGCCCAAAACCACCAAGAGTCGA	290
Qy	241	GAGGTGAAAT	GAGCACCCGGGGCCGATTCCAGTCTACTGGGATCCGCCAAGGGGAAC	300
Db	291	GAGGTGAAAT	GAGCACCCGGGGCCGATTCCAGTCTACTGGGATCCGCCAAGGGGAAC	350
Qy	301	TGCTCCTTGT	GATCAGAGCGGCAGATGCAGGATGAGTACAGTACTTCTTCGGGTG	360
Db	351	TGCTCCTTGT	GATCAGAGCGGCAGATGCAGGATGAGTACAGTACTTCTTCGGGTG	410
Qy	361	GAGAGGAAGC	TATGTGAGATAAATTTCATGAACGATGGTTCCTTTCAAAGTAACA	420
Db	411	GAGAGGAAGC	TATGTGAGATAAATTTCATGAACGATGGTTCCTTTCAAAGTAACA	470
Qy	421	GTGCTCAGCTT	CAGCCCCAGACCCAGGACCAACAACCGACCTCACTGCCATGTGGAC	480
Db	471	GTGCTCAGCTT	CAGCCCCAGACCCAGGACCAACAACCGACCTCACTGCCATGTGGAC	530
Qy	481	TTCTCCAGAAG	GGTGTGAGCGCACAGAGACCGTCCGACTCCGTGTGGCTATGCCCCC	540
Db	531	TTCTCCAGAAG	GGTGTGAGCGCACAGAGACCGTCCGACTCCGTGTGGCTATGCCCCC	590
Qy	541	AGAGACCTTGT	TATCAGCATTTACGTGCACAACCGCCCTGGAGCCCCAGCCCCAG	600
Db	591	AGAGACCTTGT	TATCAGCATTTACGTGCACAACCGCCCTGGAGCCCCAGCCCCAG	650
Qy	601	GGAAATGTC	CATACCTGGAGCCAAAAGGCCAGTTCCTGCGGCTCCTGTGTGCTGCT	660
Db	651	GGAAATGTC	CATACCTGGAGCCAAAAGGCCAGTTCCTGCGGCTCCTGTGTGCTGCT	710
Qy	661	GACAGCAGC	CCCCCTGCCACACTGAGTGGGTCTCTGCAGAACAGAGTCTCTCTCGTCC	720
Db	711	GACAGCAGC	CCCCCTGCCACACTGAGTGGGTCTCTGCAGAACAGAGTCTCTCTCGTCC	770
Qy	721	CATCCCTGG	GGGCCCTTAGACCCCTGGGCTGAGGTGCCCGGGGTGAAGGCTGGGGANTCA	780
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QY 419 ----- 418
DB 538 GCCCTGACTCAGAAAGCCTGATGTTACATCCCGAGACCTTGAGGCGCGGACGCGGTG 597
QY 419 ----- 418
DB 598 ACGGTATCTGTGTGTTAACTGGGCTTTGAGGAATGTCCACCCCTCTTTCTCTCTGG 657
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DB 658 ACGGGGCTGCCCTCTCTCTCCAGGAACCAACACGACCTCCACATCTCTCAGTCTC 717
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DB 718 AGCTTCAGGCCAGACCCAGGACCAACACACGACCTCACCCTGCCATGTGACTTCTCC 777
QY 487 AGAAGGGTGTGAGCGCACAGAGACCGTCCGACTCCGTTGCTGCTTATGCCCCCAGAGAC 546
DB 778 AGAAGGGTGTGAGCGCACAGAGACCGTCCGACTCCGTTGCTGCTTATGCCCCCAGAGAC 837
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DB 838 CTGTTTATCAGCATTTACGTGACACACCGGACCTCTGAGCCGCCAGCCACGAGAAAT 897
QY 607 GTCCCATACCTGGAAGCCCAAAAGGCGAGTCTCTGGGCTCTCTGCTGCTGCTGACAGC 666
DB 898 GTCCCATACCTGGAAGCCCAAAAGGCGAGTCTCTGGGCTCTCTGCTGCTGCTGACAGC 957
QY 667 CAGCCCTCTGCACTGAGGTGGTCTCTGAGAAAGAGTCTCTCTCTCTCTCTCTCTCTCC 726
DB 958 CAGCCCTCTGCACTGAGGTGGTCTCTGAGAAAGAGTCTCTCTCTCTCTCTCTCTCTCC 1017
QY 727 TGGGGCTTACACCTCTGGGCTGGAGCTCTCCGGGTGAAGCTGGGATTCAGGGCGC 786
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QY 787 TACACCTGCCAGCGGAGAACAGGCTTGGCTCCAGAGCGAGCCCTTGGACCTCTCTGTG 846
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QY 907 AACCTTGGAAACGCGAGCTCTCTCCAGTACTGAGGGGCCAAAGCCTGTGCTGTGT 966
DB 1198 AACCTTGGAAACGCGAGCTCTCTCCAGTACTGAGGGGCCAAAGCCTGTGCTGTGT 1257
QY 967 GTCCACACAGACGCGCCCGAGCGCTGAGCTGAGCTGAGCCAGAGGGGACAGGTTCTGAGC 1026
DB 1258 GTCCACACAGACGCGCCCGAGCGCTGAGCTGAGCTGAGCCAGAGGGGACAGGTTCTGAGC 1317
QY 1027 CCCTCCAGCGCTCAGACCCCGGGTCTCTGAGCTGCTCGGGTCAAGTGGAGCAGAA 1086
DB 1318 CCCTCCAGCGCTCAGACCCCGGGTCTCTGAGCTGCTCGGGTCAAGTGGAGCAGAA 1377
QY 1087 GGAGAGTTCACCTCCAGCTGCGACCCCACTGGGCTCCAGACAGCTCTCTCAGCCTC 1146
DB 1378 GGAGAGTTCACCTCCAGCTGCGACCCCACTGGGCTCCAGACAGCTCTCTCAGCCTC 1437
QY 1147 TCGGTGACTACTCCCGAGCTCTGCGCCCTCTGCTCTGCTGGAGGCTGAGGCTG 1206
DB 1438 TCGGTGACTACTCCCGAGCTCTGCGCCCTCTGCTCTGCTGGAGGCTGAGGCTG 1497
QY 1207 CACTGCACTCTCTCTCCAGCGAGCCCGCCCTCTCTGCGCTGGTGGTGGGAG 1266
DB 1498 CACTGCACTCTCTCTCCAGCGAGCCCGCCCTCTCTGCGCTGGTGGTGGGAG 1557
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DB 1558 GAGCTGCTGGAGGGGACAGCAGCAGGACTCTCTGAGGTCACCCCGCTCAGCCGG 1617

QY 1327 CCCTGGGCAACAGCTCCCTGAGCTCCATGGAGGGCTCAGCTCCGGCTCAGGCTCCGC 1386
DB 1618 CCCTGGGCAACAGCTCCCTGAGCTCCATGGAGGGCTCAGCTCCGGCTCAGGCTCCGC 1677
QY 1387 TGTGAGGCTCGAAACGTCCATGGGGCCAGAGTGGATCCATCTCTGAGCTGCCAGATAAG 1446
DB 1678 TGTGAGGCTCGAAACGTCCATGGGGCCAGAGTGGATCCATCTCTGAGCTGCCAGATAAG 1737
QY 1447 AAGGACTCATCTCAACGGCATTTCTCAACGGAGCTTTCTGGGAAATCGGCATCACGGCT 1506
DB 1738 AAGGACTCATCTCAACGGCATTTCTCAACGGAGCTTTCTGGGAAATCGGCATCACGGCT 1797
QY 1507 CTCTCTTTCTCTGCTGCGCTGATCATCATGAGATTTACCGAAGAGACGACTCAG 1566
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QY 1687 CGGACCCCTCTTCCAGAGTGTCTCCCGCACAGCAGATCTCTGGATTAATCAATGTG 1746
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DB 2098 AGCCAAAGAGAGTCCATTTATGCCAGCTCAACTTCCAGGCGTCCAGCCAGGCTGAG 2157
QY 1867 GCCCGATGCCAGGCGCACCCAGCGGATTTATGAGAAGTCAAGTTCCTCAA 1917
DB 2158 GCCCGATGCCAGGCGCACCCAGCGGATTTATGAGAAGTCAAGTTCCTCAA 2208

RESULT 7

AF301007 3012 bp mRNA linear PRI 26-JUL-2002
LOCUS Homo sapiens sialic acid-binding immunoglobulin-like lectin 10

DEFINITION

AF301007
AF301007 (SIGLEC10) mRNA, complete cds.

ACCESSION

AF301007

VERSION

AF301007.1

KEYWORDS

GI:21956185

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1. (bases 1 to 3012)

Whitney, G.S., Wang, S., Chang, H., Cheng, K.-Y., Liu, P., Zhou, X.D.,

Van, W.P. and Longphre, M.

A new Siglec family member, SIGLEC10, is expressed in cells of the

immune system and has signaling properties similar to CD33

Unpublished

2. (bases 1 to 3012)

Longphre, M., Whitney, G.S., Wang, S., Chang, H. and Van, W.P.

Direct Submission

Submitted (29-AUG-2000) Immunology Department, Bristol-Myers Squibb

Pharmaceutical Research Institute, Route 206 and Province Line

Road, Princeton, NJ 08543-4000, USA

Location/Qualifiers

1. .3012

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/chromosome="19"

/map="19q13.33-q13.41"

1. .3012

gene

CDS	/gene="SIGLEC10" 118..2211 /gene="SIGLEC10" /codon_start=1 /product="sialic acid-binding immunoglobulin-like lectin 10" /protein_id="AA083254.1" /db_xref="GI:21956186" /translation="MGLPILLSLLGGSQAMDRFWIRVOESVMVPEGLCISVPCSFSS YPRDWTGSTPAYVNFKAATETTKGAPVATNHSREVEMSTRGRQLTGDPAKGNCS LVIRDAQMDQESQYFPRVERGSVRYNFMNDGFLLKVTALTQKPDVYIETEPGQPV TVICVFNWAECEPSPFSWIGALSQGTFTISHFSVLSTFPRQDNIDTLDCHVD FSKRGVATXLRVAYAPRDLVISISRDNTALPEPQGNVPYVLEAKQKGFRLLC AADSQPPATLWLNRLSSHPWPRPLGLPVGKAGDSRYTCTRAENRLSQOR ALDLSVQPPENLRVMSQANRTVLENGTSLPVGOSLCLVCTVTHSSPPARLSW TORGVLSPSPDPGVLELPRVQVEHEGFTCHARPLGSHQVLSLVSHVSPKLLG PSCSWAEGHLHSCSSQASPAPSLRWLGELELGNSSQDSFVTSVAGPWANSSLS LHGGLSGELPLRCANVHCAQSGSILQLPDKGLISTAFPSNGAFILGITALFLCL ALLIMKLPKRITETPRFRSHSTILDYINVVPTAGPLAQRNOKATPNSPRTPPL PPGAPSPESKXKQKQVQLPSPFPKPSSTQAPESQBELHYATLNFPGVRRPEAR MPKGTQADYAEVRFQ"																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
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D	b	1569	GAGCTGCTGGAGGGGAACAGCAGCGCAGGAGACTCTTCGTGAGGTCAACCCCGAGCTCAGCCGGG	1628
Q	y	1327	CCCTGGGCCAAACAGCTCCCTCAGGCCTCATGAGAGGGTTCAGCTCCGGCCTCAGGCTCCGC	1386
D	b	1629	CCCTGGGCCAAACAGCTCCCTCAGGCCTCATGAGAGGGTTCAGCTCCGGCCTCAGGCTCCGC	1688
Q	y	1387	TGTGAGGCTTGGAAGTTCCATGGGGCCAGAGTGGATCCATCTCTGAGCTGCCAGATAAG	1446
D	b	1689	TGTGAGGCTTGGAAGTTCCATGGGGCCAGAGTGGATCCATCTCTGAGCTGCCAGATAAG	1748
Q	y	1447	AAGGAGTCACTCTCAAAGGCAATTCTCAAAGGAGCGTTCTTGGGAATCGGCATCACGGCT	1506
D	b	1749	AAGGAGTCACTCTCAAAGGCAATTCTCAAAGGAGCGTTCTTGGGAATCGGCATCACGGCT	1808
Q	y	1507	CTTCTTTTCTCTGCTGGCCCTGATCATATGAAGATTCTAACGAGAAGACGACTCAG	1566
D	b	1809	CTTCTTTTCTCTGCTGGCCCTGATCATATGAAGATTCTAACGAGAAGACGACTCAG	1868
Q	y	1567	ACAGAAACCCGAGGCCAGGTTCTCCGGCACAGCAGATCTCTGGATTATCATCAATGTG	1626
D	b	1869	ACAGAAACCCGAGGCCAGGTTCTCCGGCACAGCAGATCTCTGGATTATCATCAATGTG	1928
Q	y	1627	GTCOCGAGCGTGCCTCCCTGGCTCAGAAGCGGAATCAGAAGCCACACCAACAGTCTCT	1686
D	b	1929	GTCOCGAGCGTGCCTCCCTGGCTCAGAAGCGGAATCAGAAGCCACACCAACAGTCTCT	1988
Q	y	1687	CGGACCCTCTTCCACAGGTGCTCCCTCCCAGAAATCAAGAGAACCCAGAAAACAG	1746
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Q	y	1747	TATCAGTTGCCAGTTTTCCAGAACCCAAATCATCCAATCAGCCCCAGAAATCCAGGAG	1806
D	b	2049	TATCAGTTGCCAGTTTTCCAGAACCCAAATCATCCAATCAGCCCCAGAAATCCAGGAG	2108
Q	y	1807	AGCCAAGAGAGCTCCATTATGCCACGCTCACTTCCAGGCGTFCAGCCAGGCTTAG	1866
D	b	2109	AGCCAAGAGAGCTCCATTATGCCACGCTCACTTCCAGGCGTFCAGCCAGGCTTAG	2168
Q	y	1867	GCCCGGATGCCAAGGCGCCAGGCGGATTATCAGAAGTCAAGTTCCAA	1917
D	b	2169	GCCCGGATGCCAAGGCGCGACCCAGCGGATTATCAGAAGTCAAGTTCCAA	2219
<hr/>				
R	E	S	U	L
RESULT	9			
AF310233				
LOCUS				
DEFINITION	AF310233	2176 bp	mRNA	linear PRI 22-MAY-2001
ACCESSION	Homo sapiens sialic acid binding immunoglobulin-like lectin 10			
VERSION	(SIGHLE10) mRNA, complete cds.			
KEYWORDS	AF310233			
SOURCE	AF310233.1 GI:14164612			
ORGANISM	Homo sapiens (human)			
REFERENCE	Homo sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
JOURNAL	Munday,J., Kerr,S., Ni,J., Cornish,A.L., Zhang,J.Q., Nicoll,G.,			
MEDLINE	Floyd,H., Mattel,M.-G., Moore,P., Liu,D. and Crocker,P.R.			
PUBMED	Identification, characterization and leucocyte expression of			
AUTHORS	Siglec-10, a novel human sialic acid-binding receptor			
TITLE	Biochem J. 355 (Pt 2), 489-497 (2001)			
JOURNAL	21181584			
MEDLINE	11284738			
PUBMED	2 (bases 1 to 2176)			
AUTHORS	Cornish,A.L., Ni,J. and Crocker,P.R.			
TITLE	Direct Submission			
JOURNAL	Submitted (02-OCT-2000) School of Biological Sciences, University			
FEATURES	of Dundee, Dow Street, Dundee DD6 8AT, Scotland, United Kingdom			
SOURCE	Location/Qualifiers			
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1147 TCCGTGACCTACTCCCGGAAAGCTGCTGGGCCCTCTCTGCTCTTGGAGGCTGAGGGTCTG 1206
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1747 TATCAGTTGCCAGTTTCCAGAAACCAATCATCTCAAGCCCGCAGATCCAGATCCAGGAG 1806
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1807 AGCCAGAGGAGCTCCATTTATGCCACGCTCAACTTCCAGGCGTCAGACCCAGGCTGAG 1866
2018 AGCCAGAGGAGCTCCATTTATGCCACGCTCAACTTCCAGGCGTCAGACCCAGGCTGAG 2077
1867 GCCCGGATGCCAAAGGCGACCCAGGCGATTTATCGAAGTCAAGTTCCAA 1917
2078 GCCCGGATGCCAAAGGCGACCCAGGCGATTTATCGAAGTCAAGTTCCAA 2128

RESULT 10
AX365518
LOCUS AX365518 2823 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 3 from Patent WO0208257.
ACCESSION AX365518
VERSION AX365518.1 GI:18697087
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Longphre, M., Chang, H. and Whitney, G.
TITLE Novel siglecs and uses thereof.
JOURNAL Patent: WO 0208257-A 3 31-JAN-2002;
BRISTOL-MYERS SQUIBB COMPANY (US)
FEATURES
1. 2823
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 78.1%; Score 1497.4; DB 6; Length 2823;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1498; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
419 CAGTCTCAGCTTCAGCCCGAGACCCAGGACCAACACCGACTCAGCTGCGCATGTGG 478
238 CAGTCTCAGCTTCAGCCCGAGACCCAGGACCAACACCGACTCAGCTGCGCATGTGG 297
479 ACTTCTCAGAAAGGCTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGCTATGCC 538
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539 CCAGAGACCTTGTATACAGCATTTTCAGTGAACACACCCAGGCTTGAGGCCCGAGCCCC 598
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 541 AGAGACCTTGTTATCAGCAATTCACGTGACACACGCGCCAGCTCCGATCCGTTGTGGCT 600
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 766 CATCCCTGGGGCCCTAGACCCCTGGGCTGGAGTCCCGGGGTGAAGGTGGGGATTCA 825
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 901 CTGGAACCTTGGGAACCGCACGTCTCTCCAGTACTGAGAGGCCCAAGCCCTGTGCTG 960
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 DEFINITION AY358337
 ACCESSION AY358337.1 GI:37181798
 VERSION FLI CDNA.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
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 REFERENCE 1 (Bases 1 to 2764)
 AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagstad,A., Vanden,R., Watanabe,C., Weiland,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.
 TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
 JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
 PUBMED 12975309
 REFERENCE 2 (bases 1 to 2764)
 AUTHORS Clark,H.F.
 TITLE Direct Submission
 JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
 FEATURES Location/Qualifiers

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Matches 1630; Conservative	0; Mismatches	2; Indels 285; Gaps 1;
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Db	706	GACAGCCAGCCCTGCTGCCACACTGAGCTGGGTCTCTGCAGAACAGAGTCTCTCTCGTCC 765
Qy	721	CATCCCTGGGGCCCTAGACCCCTGGGCTGAGAGTGCOCGGGGTGAAGGCTGGGGATCA 780
Db	766	CATCCCTGGGGCCCTAGACCCCTGGGCTGAGAGTGCOCGGGGTGAAGGCTGGGGATCA 825
Qy	781	GGGCGCTACACCTCCGAGCGGGAACAGAGCTTGGCTCCAGCAGCGAGCCCTGGAGCTC 840
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Qy	841	TCTGTGAGTATCTCTCCAGAGAACCTGAGAGTGTGTTTCCCAAGCAACAGAGCAGTC 900
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Db	1547	TCAGCCTCCATGGAGGGCTCAGCTCCGGCTCAGGCTCGCTGTGAGGCTGGAAAGTCC	1606
QY	1406	ATGGGGCCAGAGTGGATCCATCCCTGCAGTCCAGATAAGAGGAGCTCATCTCAAAGG	1465
Db	1607	ATGGGGCCAGAGTGGATCCATCCCTGCAGTCCAGATAAGAGGAGCTCATCTCAAAGG	1666
QY	1466	CATTCTCCAAAGGAGCGTTTCTGGGAATCGGATCAAGGCTCTTTTCTCTGCTGG	1525
Db	1667	CATTCTCCAAAGGAGCGTTTCTGGGAATCGGATCAAGGCTCTTTTCTCTGCTGG	1726
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1	332	17.3	2027	4	US-08-696-537A-1	Sequence 1, Appl
2	177	9.2	1488	4	US-09-620-312D-407	Sequence 407, App
3	175.4	9.1	1437	4	US-09-023-655-1029	Sequence 1029, App
4	171.4	8.9	1597	3	US-09-038-832-3	Sequence 3, Appl
5	171.4	8.9	2900	3	US-09-038-832-1	Sequence 1, Appl
6	157.2	8.2	1501	3	US-09-046-736-1	Sequence 1, Appl
7	155.2	8.1	231	4	US-09-513-999C-522	Sequence 522, App
8	152	7.9	1502	3	US-09-046-736-3	Sequence 3, Appl
9	78.4	4.1	459	4	US-08-896-537A-11	Sequence 11, Appl
10	54.8	2.9	1473	4	US-09-352-991A-5933	Sequence 5933, App
11	54.8	2.9	1809	4	US-09-352-991A-5956	Sequence 5956, App
12	54.8	2.9	2295	4	US-09-352-991A-5939	Sequence 5939, App
13	52	2.7	4059	4	US-09-739-451-560	Sequence 560, App
14	47.2	2.5	1409	6	5242798-6	Patent No. 5242798
15	45.2	2.4	861	4	US-09-252-991A-15703	Sequence 15703, A
16	44.2	2.3	1035	1	US-07-601-094-30	Sequence 30, Appl
17	44.2	2.3	1035	1	US-08-012-735-30	Sequence 30, Appl
18	44.2	2.3	1910	3	US-09-593-711A-3	Sequence 3, Appl
19	44.2	2.3	1914	1	US-07-601-094-1	Sequence 1, Appl
20	44.2	2.3	1914	1	US-08-012-735-1	Sequence 1, Appl
21	43.2	2.3	891	4	US-09-352-991A-15676	Sequence 15676, A
22	42.4	2.2	1593	4	US-09-352-991A-5394	Sequence 5394, App
23	41.6	2.2	966	4	US-09-352-991A-18451	Sequence 18451, A
24	41.6	2.2	2265	4	US-09-352-991A-18562	Sequence 18562, A
25	41.6	2.2	2532	4	US-09-252-991A-16038	Sequence 16038, A
26	41.4	2.2	417	5	US-07-808-457-22	Sequence 22, Appl
27	41.4	2.2	417	5	PCT-US93-10178-22	Sequence 22, Appl

; APPLICANT: Duclert, A.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Patent No. 6783961

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, SOFTWARE: FastSEQ for Windows Version 2.0
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, CURRENT APPLICATION DATA:
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, APPLICATION NUMBER: US/09/046,736
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, FILING DATE: 24-Nov-1998
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, CLASSIFICATION: 514
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Matches 282; Conservative 0; Mismatches 175; Indels 5; Gaps 2;

RESULT 9
US-08-896-537A-11
; Sequence 11, Application US/08896537A
; Patent No. 659088
; GENERAL INFORMATION:
; APPLICANT: NI, Jian

APPLICANT: Gentz, Reiner L.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: CD33-Like Protein
FILE REFERENCE: 1498.0480001
CURRENT APPLICATION NUMBER: US/08/896.537A
CURRENT FILING DATE: 1997-07-18
PRIOR APPLICATION NUMBER: 60/022,481
PRIOR FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 459
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ORGANISM: Homo sapiens
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US-08-896-537A-11

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QY	351	CTTTCGGGTG	GAGAGAGGAAG	CTATGTGAGA	381		
DB	184	CTTCGGGTG	GAGAGAGGAAG	GATGATAA	214		

RESULT 10
US-09-252-991A-5933/c
Sequence 5933, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 5933
LENGTH: 1473
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5933
Query Match 2.9%; Score 54.8; DB 4; Length 1473;
Best Local Similarity 50.0%; Pred. No. 0.00033;

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QY	1326	GCCTGGGGCAACAGCTCCCTGAGCTCCATGAGGGCTCAGTCCGGCTCAGGCTCCG	1385							
Db	580	CCGCGGCACATCAGCTGCGCAACTTCTGGGGCTGCCGTGAACATCTCTGCTGTTCCG	521							
QY	1386	CTGTGAGCCTTGAACGTCCATGGGGCCAGAGTGGATCCATCTCGAGCTGCCAGATAA	1445							
Db	520	CCTTTTCGCGTGTCTCTCGCGCGCGCCAGTTCCAGGATCAGCGCCAGCTCATCCAGAG	461							
QY	1446	GAAGGACTCATCTCAACGCATTTCTCAACGAGCGTTTCTGGGATCGGCATCAGGC	1505							
Db	460	CCCCACGACATCTGCGCGGGATCCCCGACACCCCTCTTCTGTGCTGGCCAGCTGGC	401							
QY	1506	TCTCTTTTCTCTGCGCTGGCCCTGATCATCATG	1539							
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RESULT 11

US-09-252-991A-5956
Sequence 5956, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 5956
LENGTH: 1809
TYPE: DNA
ORGANISM: pseudomonas aeruginosa
US-09-252-991A-5956

Query Match

Query Match	2.98;	Score 54.9;	DB 4;	Length 1809;
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QY	1326	GCCTTGGGCAACAGTCTCCCTGAGCTTCCATGAGGGCTCAGTCCGGCTCAGGCTCG	1385	
Db	1101	CCGCGGACCATCAGCGTCGGCAACTTCTGGGGCTCCGGTGAACATCTGCTGTTCGG	1160	
QY	1386	CTGTGAGGCGTGAACGTCCATGGGCGCCAGAGTGGATCCATCTGTCAGTGTCCACATAA	1445	
Db	1161	CTGTGTCGCGGTGGTCTCTCGCCGGGCCAGTTCAGGATCGACGGCCAGTCTCATCCAG	1220	
QY	1446	GAAGGACATCATCTCAACGGCATTTCCACGAGAGCGTTTCTGGGAATCGCATCAGCC	1505	
Db	1221	CCCCACGACATCGTCGCCCGGATTCGCCGACACCCCTCTTCTGGTGTCTGCCAGCTGGC	1280	
QY	1506	TCTTCTTTTCTCTGCTGGCCCTGATCATCATG	1539	
Db	1281	GCTGTCTGATCGTCAACGTTGGCGGTGAACATCATG	1314	

RESULT 12

RESULT 12
US-09-252-991A-5939
; Sequence 5939, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 5939
LENGTH: 2295
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5939

Query Match	2.3%	Score 54.8;	DB 4;	Length 2295;
Best Local Similarity	50.0%;	Pred. No. 0.00039;		
Matches 137;	Conservative 0;	Mismatches 137;	Indels 0;	Gaps 0;
Qy	1266	GGAGCTGCTGGAGGGGAAACAGACGACGAGGACTCCTTCAGGTCACCCCGAGCTCAGCCGG	1325	
Db	1183	GGTGACCTGTACGGCACCATGATCTCTGAATTCTGCACTTCGCCCGGCTCCCGGA	1242	
Qy	1326	GCCTGGGCCAAAGACTCCCTGAGCCTCCATGAGGGCTCAGTCCGGCTCAGGCTCCG	1385	
Db	1243	CCGCGGACCATCAGCGTCGGCAACTTCTGGGGGCTGCCGGTGAACATCTGTGTTCGG	1302	
Qy	1386	CTGTGAGGCGTGAAAGTGTCATCGGGGCCAGAGTGGATCCATCTGTGAGTGTGCCAGATAA	1445	
Db	1303	CTGTGTCGGGGTGGTCTCTCGCGCGGCCCAAGTTCAGAGTCCAGCGGCAGCTCATCCAGAG	1362	
Qy	1446	GAGGGACTCATCTCAACGCGATCTTCCACGAGGCGTTTCTGGGATCCGATCAGCGC	1505	
Db	1363	CCCCACGACATCGTCGCGCGATCCCCGACACCCCTTCTCGTGTCTGCCAGCCTGGC	1422	
Qy	1506	TCCTCTTTTCTCTGCTGGCCCTGATCATCATG	1539	
Db	1423	GCTGTGTCATGTCACCGTGGCGGTGAACATCATG	1456	

RESULT 13

```

RESOL 13
US-09-799-451-560
; Sequence 560, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyang
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aiding J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunding
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-Hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radojko T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948

```

SOFTWARE: pt_FL_genes Version 2.0

SEQ ID NO 560

LENGTH: 4059

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (268)..(4056)

US-09-799-451-560

Query Match

Best Local Similarity 2.7%; Score 52; DB 4; Length 4059;

Matches 152; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

586 GAGCCAGCCAGCCAGGAAATGTCCTATCTGAGAGCCCAAAAAGCCAGTTCTCTGGCG 645

2440 GCGCCCGCAACCTGCGCCTGACCTCTCTGGAGAGCCATGGCGGCGAGCTGGGCCCTG 2499

646 CTCCTCTGTGCTGTGACAGCCAGCCGCTGACACTGAGCTGGTCTCTGCAGAAACAGA 705

2500 GTACTGTGCACTGTGACAGCCGCGCCGCGCCAGCTGCGCCCTCAGCCACGCCGCTCC 2559

706 GTCCT---CTGCTCTGCTCCATTCCTGCGGCGCTTAGACCCCTGGGGCTGGAGCTGCCCGG 762

2560 CTCTTGGCTCTCTGACAGCAGCCTCTGTCTCCCAACACCTGCGCCTGGAGCTGCGAGG 2619

763 GTGAGCTGGGATTTCAGGCGCTACACTGCGAGCGGAGAACAGGCTTGGCTCCCGAG 822

2620 CCAGAGCCAGGATGAGGTTCTACAGTGTCTGCGCGAGCCCTCTGGGCCAGGCC 2679

823 CAGCGAGCCCTGGACCTCTCTGTGCACTATCTTCCAGAGAACTGAGATGATGTTTC 882

2680 AACACGCTCGAGCTGCGGCTGGAGGCTGTGGGGTGATCTGCTCGGAGGCTGCC 2739

RESULT 14

5242798-6

Patent No. 5242798

APPLICANT: SUTCLIFFE, J. GERGO

TITLE OF INVENTION: SYNTHETIC POLYPEPTIDES CORRESPONDING

TO PORTIONS OF PROTEINOLDS TRANSLATED FROM BRAIN-SPECIFIC MRNAs,

RECEPTORS, METHODS AND DIAGNOSTICS USING THE SAME

NUMBER OF SEQUENCES: 19

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/476,961

FILING DATE: 07-FEB-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 58,620

FILING DATE: 03-JUN-1987

APPLICATION NUMBER: 516,136

FILING DATE: 21-JUL-1983

SEQ ID NO:6

LENGTH: 1409

5242798-6

Query Match

Best Local Similarity 2.5%; Score 47.2; DB 6; Length 1409;

Matches 225; Conservative 0; Mismatches 253; Indels 6; Gaps 2;

938 TGGAGGGCCAAAGCCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 997

108 TAGAGGGGAGACAGTCTCCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 167

998 GCTGAGCCAGAGGGACAGTCTGTGAGCCCTCCAGCCCTCAGACCCCGGGTCTGTGG 1057

168 CCATCTTCAAGGAGAGCAGATCTGTGCGCCAGGTCATCTATGAGTCACTGCAGCTGG 227

1058 AGCTGCTCTGGGTTCAAGTGAGCAGCAAGAGAGAGTTCACCTGCGACGCTCGGCACCCAC 1117

228 AACTCCCTGAGTACGCCCCAGACGATGGGAGTACTGGTGTGTGTGTGTGTGTGTGTGTGT 287

1118 TGGGCTCCAGCAGTCTCTCTAGCCTCTCGGTGCACTACTCTCCCGAAG---CTGCTGG 1174

Db 288 ATGGCAGAGAGCCACCGCTTCAACCTGTCTGTGGAGTTTGCTCCCATATCTCTCTGG 347

QY 1175 GCGCCCTCTCTCTCTGGAGGCTGAGGCTGTGACTGAGCTGTCTCTCCAGGCCAGCC 1234

Db 348 AATCGCACTGTGACGCGGCCAGACACCGTGCAGTGTCTGTGTGTAAATCCCAACC 407

QY 1235 GCGCCCTCTCTCTCTGGTGTGGTGTGGGAGGAGCTGTCTGGAGGGAACAGCAGCCAGG 1294

Db 408 CGEAACTCTCGTGGCTTTCAGCTGCTTCCCGCAACGCTGACTGTGAACGAGACAGA 467

QY 1295 ACTCCTTCGAGGTACCCCGCAGCTCAGCCGGGCTGGGCAACAGCTCTCTGAGCTCC 1354

Db 468 GGGAGTTGTGTACTCAGAGCGCAG---CGGCTCTCTGCTCACCAGCATCTCTACGCTCC 524

QY 1355 ATGAGGGCTCAGCTCCGGCTCAGGCTCCGCTGTGAGGCTTGGAACTCCATGGGGCCC 1414

Db 525 GGGTCAAGCCCAAGCCCAACCCCGCTCATTTGTACTCCAGGAACCTCTACGGCACC 584

QY 1415 AGAG 1418

Db 585 AGAG 588

RESULT 15

US-09-252-991A-15703

Sequence 15703, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 15703

LENGTH: 861

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-15703

Query Match

Best Local Similarity 2.4%; Score 45.2; DB 4; Length 861;

Matches 186; Conservative 0; Mismatches 208; Indels 6; Gaps 1;

QY 995 TGAGCTGGAGCCAGAGGGGACAGGTTCTGAGCCCTCCAGCCCTCAGACCCCGGGTCC 1054

Db 83 TGGCCGTAGCTCTATCGAACCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 142

QY 1055 TGGAGCTGCTCTGGTTCAGTGGAGCACGAAGGAGATTCTCCTGCGCAGCTGCTGCGTCC 1114

Db 143 GCGGCTGCGCTGCAACAACTGGCGGACCGCTGATATCCCAAGAGCCCGCGCACC 202

QY 1115 CACTGGGCTCCAGCAGCTCTCTCAGCCCTCTCGTGCACCTACTCTCCCGAGCTGTGG 1174

Db 203 GCATCTCGCGAGCTGATTCGGCTCGGCTAGTGAGCCAGGACCAACACACCAGCCCT 262

QY 1175 GCGCCCTCTCTCTCTGGGAGGCTGAGGGTCTCTGCACTGCACTGCTCTCCAGCCAGCC 1234

Db 263 ACCGCTCAGCACCCCGCTGGCCG-----CGTGGGCTTCGGCTTCTCTGCTCCAGCG 316

QY 1235 GCGCCCTCTCTCTGCGCTGTGGCTTGGGAGGAGCTCTGAGGGGAGACAGCAGCCAGG 1294

Db 317 GGGTGTGATCTGTGTCCAGCGGCTGCTGACGGGCTCGCCCGGAGACCCGCGAATGG 376

QY 1295 ACTCCTTCAGGTCAACCCCGAGCTCAGCCGGGCTGGGGCCCAACAGCTCTCTGAGCTCC 1354

Db 377 TGGGCTGGGGTATTCGAAGCGGATCCAGACCTGGATCGCCAAATCCCGAGCGGCGCA 436

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61 TTCTGGATACGAGTGCAGGAGTCAGTGTGCTGCGGAGGCGCTGTGCACTCTCTGTGCCC 120
118 TTCTGGATACGAGTGCAGGAGTCAGTGTGCTGCGGAGGCGCTGTGCACTCTCTGTGCCC 177
121 TGCTCTTTCTCTACCCCGACAAAGACTGACAGGGTCTACCCAGCTTATGCTACTGG 180
178 TGCTCTTTCTCTACCCCGACAAAGACTGACAGGGTCTACCCAGCTTATGCTACTGG 237
181 TTCAAAGCAGTACTGAGACAACCAAGGCTCTCTGTGCGCCACAACCAACAGAGTCGA 240
238 TTCAAAGCAGTACTGAGACAACCAAGGCTCTCTGTGCGCCACAACCAACAGAGTCGA 297
241 GAGGTGAATATGAGCAACCCGGGGCCGATCCAGTCTCATCTGGGATCCCGCAAGGGGAAC 300
298 GAGGTGAATATGAGCAACCCGGGGCCGATCCAGTCTCATCTGGGATCCCGCAAGGGGAAC 357
301 TGCTCTTTGCTGATCAGAGCGGCGAGATCAGAGTGAAGTACAGTACTTCTTTCGGGTG 360
358 TGCTCTTTGCTGATCAGAGCGGCGAGATCAGAGTGAAGTGAAGTACTTCTTTCGGGTG 417
361 GAGAGGAAGTATGTAGATATAATTTTCATGAACGATGGTCTTCTTAAAGTAACA 420
418 GAGAGGAAGTATGTAGATATAATTTTCATGAACGATGGTCTTCTTAAAGTAACA 477
421 GTGCTGAGCTTCAGCCCGACAGCCCGAGGACCAACACCGAGCTCAGCTGCCATGTGGAC 480
478 GTGCTGAGCTTCAGCCCGACAGCCCGAGGACCAACACCGAGCTCAGCTGCCATGTGGAC 537
481 TTCTCCAGAAAGGTTGTGAGCGCACAGAGGACCGTCCGACTCCGCTGTGGCTATGCCGCC 540
538 TTCTCCAGAAAGGTTGTGAGCGCACAGAGGACCGTCCGACTCCGCTGTGGCTATGCCGCC 597
541 AGAGACCTTTATCAGCATTTTCACTGACAAACAGCGCAGCCCTGAGGCGCCAGCCCCAG 600
598 AGAGACCTTTTATCAGCATTTTCACTGACAAACAGCGCAGCCCTGAGGCGCCAGCCCCAG 657
601 GGAATCTCCATACCTGGAAGCCCAAAAGGCCAGTTCTCTGGGCTCTCTGTGCTGCT 660
658 GGAATCTCCATACCTGGAAGCCCAAAAGGCCAGTTCTCTGGGCTCTCTGTGCTGCT 717
661 GACAGCAGCCCTTGCACACTGAGTGGTCTCTGAGAAACAGAGTCTCTCTCTGCTC 720
718 GACAGCAGCCCTTGCACACTGAGTGGTCTCTGAGAAACAGAGTCTCTCTCTGCTC 777
721 CATCCCTGGGCGCTAGACCCCTGGGCGTGGAGTCTCCGCGGTGAAGCTGGGATTCA 780
778 CATCCCTGGGCGCTAGACCCCTGGGCGTGGAGTCTCCGCGGTGAAGCTGGGATTCA 837
781 GGGCGCTTACACCTGCCAGCGGAGAACAGCTTTGGCTCCAGCAGGAGCCCTTGGACCTC 840
838 GGGCGCTTACACCTGCCAGCGGAGAACAGCTTTGGCTCCAGCAGGAGCCCTTGGACCTC 897
841 TCTGTGAGTATCTCCAGAGAACCTGAGAGTGAATGTTTCCCAAGCAACAGGACAGTC 900
898 TCTGTGAGTATCTCCAGAGAACCTGAGAGTGAATGTTTCCCAAGCAACAGGACAGTC 957
901 CTGGAACACCTTGGGAACGGCAGTCTCTCCAGTACTGAGGGGCCAAAGCCCTGTGCTG 960
958 CTGGAACACCTTGGGAACGGCAGTCTCTCCAGTACTGAGGGGCCAAAGCCCTGTGCTG 1017
961 GTCTGTGTCAACACAGAGCCCGCCAGCGAGCTGAGTGGAGCCAGAGGGGACAGGTT 1020
1018 GTCTGTGTCAACACAGAGCCCGCCAGCGAGCTGAGTGGAGCCAGAGGGGACAGGTT 1077
1021 CTGAGCCCTTCCAGAGCCCTCAGACCCCGGGTCTCTGAGTCTGCTCGGTTCAAGTGGAG 1080
1078 CTGAGCCCTTCCAGAGCCCTCAGACCCCGGGTCTCTGAGTCTGCTCGGTTCAAGTGGAG 1137
1081 CAGGAAGGAGATTACCTGCCAGCTGGGACCCCACTGGGCTCCAGACAGCTCTCTCTC 1140
1138 CAGGAAGGAGATTACCTGCCAGCTGGGACCCCACTGGGCTCCAGACAGCTCTCTCTC 1197

1141 AGCCTCTCCGTGCACTACTCCCCGAAAGCTGTGGGCCCCCTCTCTCTCTGGAGGCTGAG 1200
1198 AGCCTCTCCGTGCACTACTCCCCGAAAGCTGTGGGCCCCCTCTCTCTCTGGAGGCTGAG 1257
1201 GGTCTGCACTGCAAGTGTCTCTCCAGGCCAGCCGGGCCCCCTCTCTCTGGGTGTGGCTT 1260
1258 GGTCTGCACTGCAAGTGTCTCTCCAGGCCAGCCGGGCCCCCTCTCTCTGGGTGTGGCTT 1317
1261 GGGGAGAGAGCTGCTGGAGGGGAACAGCAGCCAGAGCTCTCTCGAGGTCAACCCAGGTCA 1320
1318 GGGGAGAGAGCTGCTGGAGGGGAACAGCAGCCAGAGCTCTCTCGAGGTCAACCCAGGTCA 1377
1321 GCGGGCCCTGGGCGCAACAGCTCTCTGAGCTCTCATGAGGGCTCAGCTCCGGCTCAGG 1380
1378 GCGGGCCCTGGGCGCAACAGCTCTCTGAGCTCTCATGAGGGCTCAGCTCCGGCTCAGG 1437
1381 CTCGCTGTGAGGCTTGAACGTCTCATGGGCCCCAGAGTGGATCCATCTCTGAGCTGCCA 1440
1438 CTCGCTGTGAGGCTTGAACGTCTCATGGGCCCCAGAGTGGATCCATCTCTGAGCTGCCA 1497
1441 GATAAGAGAGCTCATCTCAACGGCATTTCTCAACGGAGGCTTTCTGGGATCGGCAATC 1500
1498 GATAAGAGAGCTCATCTCAACGGCATTTCTCAACGGAGGCTTTCTGGGATCGGCAATC 1557
1501 ACGCTCTCTTTCTCTCTGCTCTGCTGCTGATCATCATGAATTTCTACCGAAGAGACGG 1560
1558 ACGCTCTCTTTCTCTCTGCTCTGCTGCTGATCATCATGAATTTCTACCGAAGAGACGG 1617
1561 ACTCAGACAGAAACCCCGAGCCCGAGCTTTCTCCGGCACAGCAGATCTCTGGATTAATC 1620
1618 ACTCAGACAGAAACCCCGAGCCCGAGCTTTCTCCGGCACAGCAGATCTCTGGATTAATC 1677
1621 AATGTGTCGAGGCTGCGCCCTGCTCAGAGCGGATCAGAAAGCCACACACCAAC 1680
1678 AATGTGTCGAGGCTGCGCCCTGCTCAGAGCGGATCAGAAAGCCACACACCAAC 1737
1681 AGTCTCTCGAGCCCTCTTCCACAGGCTGCTCCCTCCCGAATCAAAAGAACACGAAA 1740
1738 AGTCTCTCGAGCCCTCTTCCACAGGCTGCTCCCTCCCGAATCAAAAGAACACGAAA 1797
1741 AAGCAGTATCAGTTGCCAGTTTCCAGAACCCCAATCATCTCACTCAAGCCCGAGATCC 1800
1798 AAGCAGTATCAGTTGCCAGTTTCCAGAACCCCAATCATCTCACTCAAGCCCGAGATCC 1857
1801 CAGGAGCCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCAGGCGTCAGACCCAGG 1860
1858 CAGGAGCCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCAGGCGTCAGACCCAGG 1917
1861 CCTGAGCCCGGATGCCCAAGGGCACCCAGCGGATTATGCAAGTCAAGTTCCAA 1917
1918 CCTGAGCCCGGATGCCCAAGGGCACCCAGCGGATTATGCAAGTCAAGTTCCAA 1974

RESULT 2

US-09-836-353A-15
; Sequence 15, Application US/09836353A
; Publication No. US20030129685A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P1
; CURRENT APPLICATION NUMBER: US/09/836,353A
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 15
; LENGTH: 2295

TYPE: DNA
ORGANISM: Homo sapiens
US-09-836-353A-15

Query Match 99.5%; Score 1907.4; DB 10; Length 2295;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1911; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 1 ATGCTACTGCCACTGTCTGCTCTCGCTGCTGGGGGGTCCAGGCTATGATGGGGA 60
DB 58 ATGCTACTGCCACTGTCTGCTCTCGCTGCTGGGGGGTCCAGGCTATGATGGGGA 117
QY 61 TTCTGTGATACGAGTGAGGAGTCAAGTATGCTGCTGGAGGGCTGTGCAATCTCTGTGCC 120
DB 118 TTCTGTGATACGAGTGAGGAGTCAAGTATGCTGCTGGAGGGCTGTGCAATCTCTGTGCC 177
QY 121 TGCTCTTTCTCTACCCCGCAAGAAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAG 180
DB 178 TGCTCTTTCTCTACCCCGCAAGAAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAG 237
QY 181 TTCAAAGCAGTGTGAGCAACCAAGAGTGTCTGTGGCCACAAACCAAGAGTCAAG 240
DB 238 TTCAAAGCAGTGTGAGCAACCAAGAGTGTCTGTGGCCACAAACCAAGAGTCAAG 297
QY 241 GAGGTGGAATGAGCAACCCGGGGCCGATTCAGTCACTGGGATCCCGCCAAAGGGGAAC 300
DB 298 GAGGTGGAATGAGCAACCCGGGGCCGATTCAGTCACTGGGATCCCGCCAAAGGGGAAC 357
QY 301 TGCTCTCTGTGATCAGAGCGGAGATGAGGATGAGTCAAGTCACTCTCTGGGGT 360
DB 358 TGCTCTCTGTGATCAGAGCGGAGATGAGGATGAGTCAAGTCACTCTCTGGGGT 417
QY 361 GAGAGGAGAGTGTATGAGATATAATTCATGAGCAGTGGGTCTCTTCTAAAGTAACA 420
DB 418 GAGAGGAGAGTGTATGAGATATAATTCATGAGCAGTGGGTCTCTTCTAAAGTAACA 477
QY 421 GTGCTCAGCTTACGCGCCAGACCCAGGACCAACACCGACCTCACCTGCTATGGAC 480
DB 478 GTGCTCAGCTTACGCGCCAGACCCAGGACCAACACCGACCTCACCTGCTATGGAC 537
QY 481 TTCTCAGAAAGGTTGAGCGCACAGAGACCGTCCGACTCGGTGGCTATGCCGCC 540
DB 538 TTCTCAGAAAGGTTGAGCGCACAGAGACCGTCCGACTCGGTGGCTATGCCGCC 597
QY 541 AGAGACCTTGTATCAGCAATTCACGTGACAAACACCGACCGCTGAGCCCGCCAG 600
DB 598 AGAGACCTTGTATCAGCAATTCACGTGACAAACACCGACCGCTGAGCCCGCCAG 657
QY 601 GGAATGTCCATACCTGGAGCCCAAGAGCCAGTTCCTGGGCTCTCTGTGCTGCT 660
DB 658 GGAATGTCCATACCTGGAGCCCAAGAGCCAGTTCCTGGGCTCTCTGTGCTGCT 717
QY 661 GACAGCCAGCCCTGCGCACTGAGTGGGTCTCTGAGAACAGAGTCTCTCTGCTCC 720
DB 718 GACAGCCAGCCCTGCGCACTGAGTGGGTCTCTGAGAACAGAGTCTCTCTGCTCC 777
QY 721 CATCCCTGGGCTAGACCCCTGGGCTGAGCTGCGGGGTGAAGCTGGGATTC 780
DB 778 CATCCCTGGGCTAGACCCCTGGGCTGAGCTGCGGGGTGAAGCTGGGATTC 837
QY 781 GGGCGCTACACCTGCGGAGGAGAACAGGCTTGGCTCCAGCAGCGAGCCCTGGACCTC 840
DB 838 GGGCGCTACACCTGCGGAGGAGAACAGGCTTGGCTCCAGCAGCGAGCCCTGGACCTC 897
QY 841 TCTGTGAGTATCTCTCAGAGAACCTGAGAGTATGTTTCCCAAGCAACAGGACAGTC 900
DB 898 TCTGTGAGTATCTCTCAGAGAACCTGAGAGTATGTTTCCCAAGCAACAGGACAGTC 957
QY 901 CTGGAACCTTGGGAACGCAAGTCTCTCCAGTACTGGAGGGCCAAAGCCCTGCTCC 960
DB 958 CTGGAACCTTGGGAACGCAAGTCTCTCCAGTACTGGAGGGCCAAAGCCCTGCTCC 1017
QY 961 GTCTGTGTCACACAGCAGCCCGCCCGAGCGCTGAGTGGACCCAGAGGGGACAGGTT 1020
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RESULT 3

US-09-910-600-2
; Sequence 2, Application US/09910600
; Publication No. US20030036631A1
; GENERAL INFORMATION:
; APPLICANT: Longphre, Malinda
; APPLICANT: Chang, Han
; APPLICANT: Whitney, Gena
; TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF

```
DB 1018 GTCTGTGTCAACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAGGTT 1077
QY 1021 CTGAGCCCTCCAGAGCCCTCAGACCCCGGGGTCTCTGAGCTGCCTCGGTTCAAGTGGAG 1080
DB 1078 CTGAGCCCTCCAGAGCCCTCAGACCCCGGGGTCTCTGAGCTGCCTCGGTTCAAGTGGAG 1137
QY 1081 CACGAAGGAGAGTTCACCTGCCAGCTCGGCACCACTGGGCTCCAGCAGCTCTCTCTC 1140
DB 1138 CACGAAGGAGAGTTCACCTGCCAGCTCGGCACCACTGGGCTCCAGCAGCTCTCTCTC 1197
QY 1141 AGCCTCTCCGTCACCTACTCCCGAAGTGTCTGGGCCCCCTCTCTCTCTCTGGAGGCTGAG 1200
DB 1198 AGCCTCTCCGTCACCTACTCCCGAAGTGTCTGGGCCCCCTCTCTCTCTCTGGAGGCTGAG 1257
QY 1201 GGTCTGCACTGACGTCTCTCCAGCCAGCCGCGCCCTCTCTCTCTCTCTCTCTCTCTCT 1260
DB 1258 GGTCTGCACTGACGTCTCTCCAGCCAGCCGCGCCCTCTCTCTCTCTCTCTCTCTCTCT 1317
QY 1261 GGGAGGAGAGTCTCTGGAGGGGAACAGCAGCCAGGACTCTCTCTGAGTCAACCCAGCTCA 1320
DB 1318 GGGAGGAGAGTCTCTGGAGGGGAACAGCAGCCAGGACTCTCTCTGAGTCAACCCAGCTCA 1377
QY 1321 CCGGGCCCTGGGCAACAGCTCTCTGAGCTCCATGGAGGGCTCAGCTCCGGCTCAGG 1380
DB 1378 CCGGGCCCTGGGCAACAGCTCTCTGAGCTCCATGGAGGGCTCAGCTCCGGCTCAGG 1437
QY 1381 CTCTGCTGTGAGGCTGTGAACTGCTATGGGGCCAGAGTGGATCCATCTCTCAGCTGCCA 1440
DB 1438 CTCTGCTGTGAGGCTGTGAACTGCTATGGGGCCAGAGTGGATCCATCTCTCAGCTGCCA 1497
QY 1441 GATAAGAGGAGTCACTCAACGGCATTTCTCAACGGAGGCTTTCTGGGAATCGGATC 1500
DB 1498 GATAAGAGGAGTCACTCAACGGCATTTCTCAACGGAGGCTTTCTGGGAATCGGATC 1557
QY 1501 ACGGCTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1560
DB 1558 ACGGCTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1617
QY 1561 ACTCAGACAGAAACCCCGAGGCCAGGTTCTCCGGCACAGCAGATCTCTGGATTAATC 1620
DB 1618 ACTCAGACAGAAACCCCGAGGCCAGGTTCTCCGGCACAGCAGATCTCTGGATTAATC 1677
QY 1621 AATGTGTTCCGAGCGGCTGGGCCCTGGCTCAGAGCGGATCAGAAAGCCACACCAAC 1680
DB 1678 AATGTGTTCCGAGCGGCTGGGCCCTGGCTCAGAGCGGATCAGAAAGCCACACCAAC 1737
QY 1681 AGTCTCTCGAACCCCTCTTCCACAGGTGCTCCCTCCCGAGAAATCAAGAAAGAACAGAAA 1740
DB 1738 AGTCTCTCGAACCCCTCTTCCACAGGTGCTCCCTCCCGAGAAATCAAGAAAGAACAGAAA 1797
QY 1741 AAGCAGTATCAGTTGCGCCAGTTTCCAGAACCCAAATCATCTCAAGCCCGAGATCC 1800
DB 1798 AAGCAGTATCAGTTGCGCCAGTTTCCAGAACCCAAATCATCTCAAGCCCGAGATCC 1857
QY 1801 CAGGAGAGCCAGAGGAGTCCATTATGTCACGCTCAACTTCCAGGGCTCAGACCCAGG 1860
DB 1858 CAGGAGAGCCAGAGGAGTCCATTATGTCACGCTCAACTTCCAGGGCTCAGACCCAGG 1917
QY 1861 CTTGAGGCCCGGATGCCCAAGGCAACCCAGCGGATTTATGCAAGTCAAGTTCCAA 1917
DB 1918 CTTGAGGCCCGGATGCCCAAGGCAACCCAGCGGATTTATGCAAGTCAAGTTCCAA 1974
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FILE REFERENCE: D0003NP
CURRENT APPLICATION NUMBER: US/09/910,600
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/220,139
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 2954
TYPE: DNA
ORGANISM: Homo sapiens
OS: 910-600-2

Query Match

Best Local Similarity 97.4%; Score 1868; DB 10; Length 2954;
Matches 1868; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	50	TGGATGGAGATTCTGGATACGAGTGCAGGAGTCAGTGATGGTGGCGGAGGCTGTGCA	109
DB	1	TGGATGGAGATTCTGGATACGAGTGCAGGAGTCAGTGATGGTGGCGGAGGCTGTGCA	60
QY	110	TCTCTGTGCTGCTCTTCTCTCTACCCCGCAAGAAGTGGACAGGCTTACCCAGCTT	169
DB	61	TCTCTGTGCTGCTCTTCTCTCTACCCCGCAAGAAGTGGACAGGCTTACCCAGCTT	120
QY	170	ATGGCTACTGGTTCAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	229
DB	121	ATGGCTACTGGTTCAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	180
QY	230	ACCAGAGTCAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	289
DB	181	ACCAGAGTCAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	240
QY	290	CCAGAGGAGTCTCTCTGGTATCAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGT	349
DB	241	CCAGAGGAGTCTCTCTGGTATCAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGT	300
QY	350	TCTTTTGGGTGGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	409
DB	301	TCTTTTGGGTGGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	360
QY	410	TAAAGTAAAGTCTCAGCTTCAAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGT	469
DB	361	TAAAGTAAAGTCTCAGCTTCAAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGT	420
QY	470	GCCATGTGGACTTCTCCAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	529
DB	421	GCCATGTGGACTTCTCCAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	480
QY	530	CCTATGCCCCCAGAGACTTGTATCAGCATTTTCAAGTGAAGTGAAGTGAAGT	589
DB	481	CCTATGCCCCCAGAGACTTGTATCAGCATTTTCAAGTGAAGTGAAGTGAAGT	540
QY	590	CCAGAGCCAGAGAGTTCCTATCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGT	649
DB	541	CCAGAGCCAGAGAGTTCCTATCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGT	600
QY	650	TCTGTGCTGTCAGAGAGTCCCTGCACTGAGCTGGTCTCTGAGAGAGAGTCC	709
DB	601	TCTGTGCTGTCAGAGAGTCCCTGCACTGAGCTGGTCTCTGAGAGAGAGTCC	660
QY	710	TCTCTGCTGCTATCCCTGGGGGCTTAGACCTCTGGGGTGGAGCTGCCGGGGTGAAG	769
DB	661	TCTCTGCTGCTATCCCTGGGGGCTTAGACCTCTGGGGTGGAGCTGCCGGGGTGAAG	720
QY	770	CTGGGATTCAGAGGCTTACCTCTGCGGAGAGTGAAGTGAAGTGAAGTGAAGT	829
DB	721	CTGGGATTCAGAGGCTTACCTCTGCGGAGAGTGAAGTGAAGTGAAGTGAAGT	780
QY	830	CCCTGAGACTCTCTGTGAGTATCTCTCAGAGAGTGAAGTGAAGTGAAGTGAAGT	889
DB	781	CCCTGAGACTCTCTGTGAGTATCTCTCAGAGAGTGAAGTGAAGTGAAGTGAAGT	840

QY	890	ACAGGACAGTCTCTGGAAAAACCTTGGAAACAGGACGTCTCTCCAGTACTTGAGGGCCAAA	949
DB	841	ACAGGACAGTCTCTGGAAAAACCTTGGAAACAGGACGTCTCTCCAGTACTTGAGGGCCAAA	900
QY	950	SCCTGTGCTGCTGT	1009
DB	901	SCCTGTGCTGCTGT	960
QY	1010	GGGACAGGTTCTGAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCT	1069
DB	961	GGGACAGGTTCTGAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCT	1020
QY	1070	TTCAGTGGAGCAGAGGAGTTCACCTGCGAGCTTCCAGGCTTCCAGGCTTCCAGGCT	1129
DB	1021	TTCAGTGGAGCAGAGGAGTTCACCTGCGAGCTTCCAGGCTTCCAGGCTTCCAGGCT	1080
QY	1130	ACGTCTCTCTCAGGCTTCTCCGTGCACTACTCCCGAAGCTTCTCCCGAAGCTTCTCC	1189
DB	1081	ACGTCTCTCTCAGGCTTCTCCGTGCACTACTCCCGAAGCTTCTCCCGAAGCTTCTCC	1140
QY	1190	GGGAGGCTGAGGCTTCTGCACTGCACTGCTCTCCAGGCTTCCAGGCTTCCAGGCT	1249
DB	1141	GGGAGGCTGAGGCTTCTGCACTGCACTGCTCTCCAGGCTTCCAGGCTTCCAGGCT	1200
QY	1250	GCTGTGCTTGGGAGGAGTCTGCTGGAGGAAACAGCAGCAGGAGTCTCTTCGAGTCA	1309
DB	1201	GCTGTGCTTGGGAGGAGTCTGCTGGAGGAAACAGCAGCAGGAGTCTCTTCGAGTCA	1260
QY	1310	CCCCAGCTAGCGGGCTTGGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCT	1369
DB	1261	CCCCAGCTAGCGGGCTTGGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCT	1320
QY	1370	CCGCTCAGGCTCCGCTGTGAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCT	1429
DB	1321	CCGCTCAGGCTCCGCTGTGAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCT	1380
QY	1430	TGAGCTGCCAGATGAAGAGGACTCATCTCAACGGGATTTCTCAACGGGATTTCTGG	1489
DB	1381	TGAGCTGCCAGATGAAGAGGACTCATCTCAACGGGATTTCTCAACGGGATTTCTGG	1440
QY	1490	GAATGGGATCAGGCTTCTTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1549
DB	1441	GAATGGGATCAGGCTTCTTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1500
QY	1550	CGAAGAGCAGGACTCAGACAGAAACCCGAGGCTTCCAGGCTTCCAGGCTTCCAGGCT	1609
DB	1501	CGAAGAGCAGGACTCAGACAGAAACCCGAGGCTTCCAGGCTTCCAGGCTTCCAGGCT	1560
QY	1610	TGGATTATCATGTGTGCTCCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1669
DB	1561	TGGATTATCATGTGTGCTCCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1620
QY	1670	CCACACCAACAGTCTCGGACCTTCTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCT	1729
DB	1621	CCACACCAACAGTCTCGGACCTTCTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCT	1680
QY	1730	AGAACCAAGAAACAGTATCAGTTGCCAGTTTCCAGGCTTCCAGGCTTCCAGGCT	1789
DB	1681	AGAACCAAGAAACAGTATCAGTTGCCAGTTTCCAGGCTTCCAGGCTTCCAGGCT	1740
QY	1790	CCCCAGATCCAGGAGCAGAGGAGTCCATTTGCGAGCTTCCAGGCTTCCAGGCT	1849
DB	1741	CCCCAGATCCAGGAGCAGAGGAGTCCATTTGCGAGCTTCCAGGCTTCCAGGCT	1800
QY	1850	TCAGACCCAGGCTTGGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCT	1909
DB	1801	TCAGACCCAGGCTTGGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCT	1860
QY	1910	AGTTCCAA 1917	
DB	1861	AGTTCCAA 1868	

1627 GTCCGAGCGCTGCCCCCTGGCTCAGAAGCGGAATCAGAAAGCCACCAACAAAGTCCT 1686
1918 GTCCGAGCGCTGCCCCCTGGCTCAGAGCGGNATCAGAAAGCCACCAACAAAGTCCT 1977
1687 CGGACCCCTCTTCCACAGAGTGTCTCCCTCCAGAAATCAAAGAAAGAACCAAGAAAGCAG 1746
1978 CGGACCCCTCTTCCACAGAGTGTCTCCCTCCAGAAATCAAAGAAAGAACCAAGAAAGCAG 2037
1747 TATCAGTTGCCAGTTTCCAGAGACCAATCATCACTCAAGCCCAAGATCCCAAGGAG 1806
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1807 AGCCAAAGAGGAGTCCATTATGCCACGCTCAACTTCCAGCGCTCAGACCCAGGCTGAG 1866
2098 AGCCAAAGAGGAGTCCATTATGCCACGCTCAACTTCCAGCGCTCAGACCCAGGCTGAG 2157
1867 GCCCGGATGCCAGGCGACCCAGGCGGATATGCAGAAATCAAGTTCCAA 1917
2158 GCCCGGATGCCAGGCGACCCAGGCGGATATGCAGAAATCAAGTTCCAA 2208

RESULT 5

US-09-910-600-27
Sequence 27, Application US/09910600
Publication No. US2003003631A1
GENERAL INFORMATION:
APPLICANT: Longphre, Malinda
APPLICANT: Chang, Han
TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
FILE REFERENCE: D0003NP
CURRENT APPLICATION NUMBER: US/09/910,600
PRIORITY FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/220,139
PRIORITY FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 3024
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: L3-995-2
US-09-910-600-27

Query Match 90.4%; Score 1733; DB 10; Length 3024;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1917; Conservative 0; Mismatches 0; Indels 174; Gaps 1;
QY 1 ATGCTACTGCACTGCTGCTCTCGCTGCTGGCGGGTCCAGGCTATGATGGAGA 60
DB 129 ATGCTACTGCACTGCTGCTCTCGCTGCTGGCGGGTCCAGGCTATGATGGAGA 188
QY 61 TTCTGATACGAGTCCAGAGTCAAGTGGTCCCGAGGCGCTGTGCACTCTGTGCCC 120
DB 189 TTCTGATACGAGTCCAGAGTCAAGTGGTGGCGGGCTGTGCACTCTGTGCCC 248
QY 121 TGCTCTTTCTTCTTACCCCGAGAGTCAAGAGTGTGCTGTGGCCACCAACCCAGAGTGA 180
DB 249 TGCTCTTTCTTCTTACCCCGAGAGTCAAGAGTGTGCTGTGGCCACCAACCCAGAGTGA 308
QY 181 TTCAAAGCAGTGAAGTCAAGAGTGTGCTGTGGCCACCAACCCAGAGTGA 240
DB 309 TTCAAAGCAGTGAAGTCAAGAGTGTGCTGTGGCCACCAACCCAGAGTGA 368
QY 241 GAGGTGAAGTGAAGTCAAGAGTGTGCTGTGGCCACCAACCCAGAGTGA 300
DB 369 GAGGTGAAGTGAAGTCAAGAGTGTGCTGTGGCCACCAACCCAGAGTGA 428
QY 301 TGCTCTTTGATGATCAGAGTCAAGAGTGTGCTGTGGCCACCAACCCAGAGTGA 360
DB 429 TGCTCTTTGATGATCAGAGTCAAGAGTGTGCTGTGGCCACCAACCCAGAGTGA 488

QY 361 GAGAGAGAGCTATGTGATATATATTTTCATGACGATGGTCTTTCTAAAGTAA-- 418
DB 489 GAGAGAGAGCTATGTGATATATATTTTCATGACGATGGTCTTTCTAAAGTAA-- 548
QY 419 ----- 418
DB 549 GCCCTGACTCAGAGCCTGATGTCTACATCCCGAGACCTCGGAGCCCGGCGACCGG 608
QY 419 ----- 418
DB 609 AGGTCATCTGTGTGTTTAACTGGGCTTTGAGAAATGCCACCCCTCTTTCTCTGG 668
QY 419 ----- 418
DB 669 AGGCGGCTGCCCTCTCTCTCCAGGAACCAACAGGACCTCCACTTCTCAGTGTCT 728
QY 427 AGCTTCAGCCCGAGACCCCGAGGACCAACACCGACCTCAGCTGCGATGTGGATCTCTCC 486
DB 729 AGCTTCAGCCCGAGACCCCGAGGACCAACACCGACCTCAGCTGCGATGTGGATCTCTCC 788
QY 487 AGAAAGGTGTGAGCGACAGAGGACCGTCCGACTTCGCTGTGGCTATGCCCCCAGAGAC 546
DB 789 AGAAAGGTGTGAGCGGACAGAGGACCGTCCGACTTCGCTGTGGCTATGCCCCCAGAGAC 848
QY 547 CTTGTTATCAGATTTTCAAGTGAACACCGCCCTTGAGGCCCCAGGCCCGAGGAAAT 606
DB 849 CTTGTTATCAGATTTTCAAGTGAACACCGCCCTTGAGGCCCCAGGCCCGAGGAAAT 908
QY 607 GTCCCATACCTGGAAGCCCAAAAGGCGGCTTCCTGGGCTCTCTGCTGTGCTGAGCAGC 666
DB 909 GTCCCATACCTGGAAGCCCAAAAGGCGGCTTCCTGGGCTCTCTGCTGTGCTGAGCAGC 968
QY 657 CAGCCCCCTGCCACACATGAGCTGGGCTCTGAGAACAGAGTCTCTCTCTGCTGCTGCTCC 726
DB 969 CAGCCCCCTGCCACACATGAGCTGGGCTCTGAGAACAGAGTCTCTCTCTGCTGCTGCTCC 1028
QY 727 TGGGGCCCTAGACCCCTGGGCTGAGCTGCCCGGGGTGAAGCTGGGATTCAGGGGCGC 786
DB 1029 TGGGGCCCTAGACCCCTGGGCTGAGCTGCCCGGGGTGAAGCTGGGATTCAGGGGCGC 1088
QY 787 TACACCTGCCAGCGGAGAACAGAGCTTTGGCTCCAGAGCGAGGACCTCTGAGCTCTCTGTG 846
DB 1089 TACACCTGCCAGCGGAGAACAGAGCTTTGGCTCCAGAGCGAGGACCTCTGAGCTCTCTGTG 1148
QY 847 CAGTATCTCTCAGAGAACCTGAGAGTGTATGTTTCCCAAGAACAGAGACAGTCTGGAA 906
DB 1149 CAGTATCTCTCAGAGAACCTGAGAGTGTATGTTTCCCAAGAACAGAGACAGTCTGGAA 1208
QY 907 AACCTTGGGAAGCGGACGCTCTCTCCAGTACTGAGGGGCCAAGGCTGTGCTGCTGTCTGT 966
DB 1209 AACCTTGGGAAGCGGACGCTCTCTCCAGTACTGAGGGGCCAAGGCTGTGCTGCTGTCTGT 1268
QY 967 GTCAACACAGAGCAGCCCCCAGGCTGAGTGGACCCAGAGGAGACAGTCTTCTGAGC 1026
DB 1269 GTCAACACAGAGCAGCCCCCAGGCTGAGTGGACCCAGAGGAGACAGTCTTCTGAGC 1328
QY 1027 CCCTCCAGGCTCTCAGACCCCGGGGTCTCTGAGCTGCTCGGCTTCAAGTGGAGACGAA 1086
DB 1329 CCCTCCAGGCTCTCAGACCCCGGGGTCTCTGAGCTGCTCGGCTTCAAGTGGAGACGAA 1388
QY 1087 GGAGAGTTACCTTGCCACGCTCGGACCCACTGGGCTCCAGAGACGCTCTCTCTCAGGCTC 1146
DB 1389 GGAGAGTTACCTTGCCACGCTCGGACCCACTGGGCTCCAGAGACGCTCTCTCTCAGGCTC 1448
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QY 1207 CACTTGCAGCTGCTCTCTCCAGGCGCAGCCCGGCGCTCTCTCTGCTGCTGCTGCTGGGAG 1266
DB 1509 CACTGCACTGCTCTCTCCAGGCGCAGCCCGGCGCTCTCTCTGCTGCTGCTGCTGGGAG 1568
QY 1267 GAGTGTCTGAGGGGGAACAGAGCGGAGTCTCTTTCAGAGTCAACCCAGCTCAGCCGGG 1326

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Db 1569 GAGCTCTGAGGGAAACAGCAGCAGGAGTCTCTTCGAGGTACCCCGAGCTCAGCCGGG 1628
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Db 1629 CCTGGGCAACAGCTCCCTGAGCTCCATGAGGGCTCAGTCCGGCTCAGGCTCCGC 1688
Qy 1387 TGTGAGCTTGAACTCCATGGGCCCCAGAGTGAATCCATCCTGAGCTGCCAGTAAG 1446
Db 1689 TGTGAGCTTGAACTCCATGGGCCCCAGAGTGAATCCATCCTGAGCTGCCAGTAAG 1748
Qy 1447 AAGGAGCTCATCTCAACGGCATTCTCCAGCGAGGCTTCTGGGAATGGCATCAGGCT 1506
Db 1749 AAGGAGCTCATCTCAACGGCATTCTCCAGCGAGGCTTCTGGGAATGGCATCAGGCT 1808
Qy 1507 CTTCTTTTCTCTGCTGGCCCTGATCATCAAGATTCTACCGAAGAGACGGACTCAG 1566
Db 1809 CTTCTTTTCTCTGCTGGCCCTGATCATCAAGATTCTACCGAAGAGACGGACTCAG 1868
Qy 1567 ACAGAAACCCGAGGCGAGGTTCTCCGGCACAGCAGCATCTGGATTACATCAATGTG 1626
Db 1869 ACAGAAACCCGAGGCGAGGTTCTCCGGCACAGCAGCATCTGGATTACATCAATGTG 1928
Qy 1627 GTCCCAAGGCTGGCCCTGGCTCAGAAAGCGAAATCAGAAAGCCACACAAACAGTCTCT 1686
Db 1929 GTCCCAAGGCTGGCCCTGGCTCAGAAAGCGAAATCAGAAAGCCACACAAACAGTCTCT 1988
Qy 1687 CGAACCCCTTCCACAGAGTGTCTCCCTCCAGAAATCAAGAAAGAACAGAAAGCGAG 1746
Db 1989 CGAACCCCTTCCACAGAGTGTCTCCCTCCAGAAATCAAGAAAGAACAGAAAGCGAG 2048
Qy 1747 TATCAGTGGCCAGTGTCCAGAAACCAATCATCCACTCAAGCCCAAGATCCAGGAG 1806
Db 2049 TATCAGTGGCCAGTGTCCAGAAACCAATCATCCACTCAAGCCCAAGATCCAGGAG 2108
Qy 1807 AGCCAGAGAGAGTCCATTATGCCAGCTCAACTTCCAGGGCTCAGACCCAGGCTGAG 1866
Db 2109 AGCCAGAGAGAGTCCATTATGCCAGCTCAACTTCCAGGGCTCAGACCCAGGCTGAG 2168
Qy 1867 GCCCGATGCCAAGGCAACCCAGGCGGATTATGCAAGTCAAGTTCCAA 1917
Db 2169 GCCCGATGCCAAGGCAACCCAGGCGGATTATGCAAGTCAAGTTCCAA 2219
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RESULT 6

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US-10-614-853-9
; Sequence 9, Application US/10614853
; Publication No. US20040138114A1
; GENERAL INFORMATION:
; APPLICANT: HILARY CHIU
; APPLICANT: KATHRYN DENNIS
; APPLICANT: SHERMAN FONG
; APPLICANT: JILL SCHOENFELD
; APPLICANT: WILLIAM WOOD
; APPLICANT: THOMAS WU
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
; FILE REFERENCE: PL973R1-US
; CURRENT APPLICATION NUMBER: US/10/614,853
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 60/394,485
; PRIOR FILING DATE: 2002-07-08
; NUMBER OF SEQ ID NOS: 28
; SEQ ID NO 9
; LENGTH: 2176
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-614-853-9
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Query Match 90.2%; Score 1729.8; DB 17; Length 2176;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1915; Conservative 0; Mismatches 2; Indels 174; Gaps 1;
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Qy 1 ATGCTACTGCCACTGCTGCTGCTCCTGCTGGGCGGGTCCAGGCTATGGATGGAGA 60
Db 38 ATGCTACTGCCACTGCTGCTGCTCCTGCTGGGCGGGTCCAGGCTATGGATGGAGA 97
Qy 61 TTCTGGATACGAGTGCAGGAGTCAATGATGTCGCGAGGCGCTGTCATCTCTGTGCC 120
Db 98 TTCTGGATACGAGTGCAGGAGTCAATGATGTCGCGAGGCGCTGTCATCTCTGTGCC 157
Qy 121 TGCTCTTTCTCTCTACCCCGACAAAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGG 180
Db 158 TGCTCTTTCTCTCTACCCCGACAAAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGG 217
Qy 181 TTCAAAGCAGTACTGAGACAAACCAAGGTGCTCTGTCGCCCAACAAACACACAGTCTGA 240
Db 218 TTCAAAGCAGTACTGAGACAAACCAAGGTGCTCTGTCGCCCAACAAACACACAGTCTGA 277
Qy 241 GAGGTGAAATAGACACCCGGGCGGATTCCAGCTCACTGGGGATCCGCCAAGGGGAAC 300
Db 278 GAGGTGAAATAGACACCCGGGCGGATTCCAGCTCACTGGGGATCCGCCAAGGGGAAC 337
Qy 301 TGCTCTTTGATGATGAGACCGCGCAGATGAGTACAGTACTTCTTTCCGGGTG 360
Db 338 TGCTCTTTGATGATGAGACCGCGCAGATGAGTACAGTACTTCTTTCCGGGTG 397
Qy 361 GAGAGGAAGCTATGTGAGATATAATTTCAATGAACGATGGGTCTTTCTAAAAAGTAA-- 418
Db 398 GAGAGGAAGCTATGTGAGATATAATTTCAATGAACGATGGGTCTTTCTAAAAAGTAA 457
Qy 419 ----- 418
Db 458 GCCCTGACTCAGAAAGCCTGATGCTCATATCCCGAGAGCCCTGGAGCCCGGCGAGCGGTG 517
Qy 419 ----- 418
Db 518 ACGGTCACTCTGTGTGTTAACTGGGCTTTGAGGAATGTCCACCCCTCTTTCTCTCTGG 577
Qy 419 ----- 426
Db 578 ACGGGGCTGCCCTCTCTCCCAAGGAACCAACCAACGACCTCCCACTTCTCAGTGTCT 637
Qy 427 AGCTTCAGCCCGACACCCCGAGACCAACACACGACCTCAGCTGCCATGTGGATCTTCC 486
Db 638 AGCTTCAGCCCGACACCCCGAGACCAACACACGACCTCAGCTGCCATGTGGATCTTCC 697
Qy 487 AGAAAGGCTGTGAGCGCACAGAGGACCGTCCGACTCCGCTGTGGCTATGCCCCAGAGAC 546
Db 698 AGAAAGGCTGTGAGCGTACAGAGGACCGTCCGACTCCGCTGTGGCTATGCCCCAGAGAC 757
Qy 547 CTTGTTATCAGATTTCAGTGACAAACACGCGAGCCCTGGAGCCCGCCAGGGAAT 606
Db 758 CTTGTTATCAGATTTCAGTGACAAACACGCGAGCCCTGGAGCCCGCCAGGGAAT 817
Qy 607 GTCCCATACCTGGAAGCCCAAGGCGAGTCTCTGCGGCTCCTCTGTGCTGCTGACAGC 666
Db 818 GTCCCATACCTGGAAGCCCAAGGCGAGTCTCTGCGGCTCCTCTGTGCTGCTGACAGC 877
Qy 667 CAGCCCTCTGCCACACTGAGTGGGTCTCTGAGAACAGAGTCTCTCTCTGCTCCATCCC 726
Db 878 CAGCCCTCTGCCACACTGAGTGGGTCTCTGAGAACAGAGTCTCTCTCTGCTCCATCCC 937
Qy 727 TCGGGCCCTAGACCCCTGGGCTGGAGCTGCCGGGTGAGGCTGGGGATTTCAGGGCGC 786
Db 938 TCGGGCCCTAGACCCCTGGGCTGGAGCTGCCGGGTGAGGCTGGGGATTTCAGGGCGC 997
Qy 787 TACACCTGCCAGCGGAGAACAGGCTTGGCTCCAGCAGCGAGCCCTGGACTCTCTCTGTG 846
Db 998 TACACCTGCCAGCGGAGAACAGGCTTGGCTCCAGCAGCGAGCCCTGGACTCTCTGTG 1057
Qy 847 CAGTATCTCCAGAAACCTGAGAGTGTGTTTCCCAAGCAACAGACAGTCTCTCGAA 906
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907 AACCTTGGAAACGGACGCTCTCTCCAGTACTGGAGGGCCAAAGCCCTGTGCTGGTCTGT 966
1118 AACCTTGGAAACGGACGCTCTCTCCAGTACTGGAGGGCCAAAGCCCTGTGCTGGTCTGT 1177
967 GTACACACAGCAGCCGCCAGCAGCTGAGCTGGAGCCAGAGGGGACAGGTTCTGAGC 1026
1178 GTACACACAGCAGCCGCCAGCAGCTGAGCTGGAGCCAGAGGGGACAGGTTCTGAGC 1237
1027 CCCTCCACAGCCTCAGACCCCGGGTCTCTGAGCTGCTCGGGTTCAAGTGGAGCAGAA 1086
1238 CCCTCCACAGCCTCAGACCCCGGGTCTCTGAGCTGCTCGGGTTCAAGTGGAGCAGAA 1297
1087 GGAGAGTTACCTGCCAGCTGGGACACCACTGGGCTCCAGCAGCTCTCTCAGGCTC 1146
1298 GGAGAGTTACCTGCCAGCTGGGACACCACTGGGCTCCAGCAGCTCTCTCAGGCTC 1357
1147 TCCGTGCACTACTCCCGAAGCTGCTGGGCCCCCTCTGCTCTCTGGAGGGCTGAGGCTCTG 1206
1358 TCCGTGCACTACTCCCGAAGCTGCTGGGCCCCCTCTGCTCTCTGGAGGGCTGAGGCTCTG 1417
1207 CACTGAGCTGCTCTCCAGGGCAGCCCGCCCCCTCTCTGCGCTGGTGGCTTGGGGAG 1266
1418 CACTGAGCTGCTCTCCAGGGCAGCCCGCCCCCTCTCTGCGCTGGTGGCTTGGGGAG 1477
1267 GAGCTGCTGGAGGGGACAGCCAGGACTCTCTGAGGTGACCCCGAGCTCAGCGGG 1326
1478 GAGCTGCTGGAGGGGACAGCCAGGACTCTCTGAGGTGACCCCGAGCTCAGCGGG 1537
1327 CCCTGGGCCAACAGCTCCCTGAGCTCCATGGAGGCTCAGCTCCGGCTCAGGCTCCCG 1386
1538 CCCTGGGCCAACAGCTCCCTGAGCTCCATGGAGGCTCAGCTCCGGCTCAGGCTCCCG 1597
1387 TGTGAGGCTTGAAGCTTCATGGGGCCAGAGTGGATCGATCTGAGCTGCCAGATAG 1446
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1658 AAGGAGTCTATCTCAAGGCAATCTCAAGCGGAGCGTTCTGGGAATCGCATCAGGCT 1717
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1807 AGCAGAGAGGCTCATATATGACGCTCACTTCCCGAGGCTCAGACCCAGGCTGAG 1866
2018 AGCAGAGAGGCTCATATATGACGCTCACTTCCCGAGGCTCAGACCCAGGCTGAG 2077
1867 GCCCGATGCCAAGGGCAGCCAGGCGGATTTATGAGAAAGTCAAGTTCCAA 1917
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RESULT 7

US-09-984-130-148

Sequence 148, Application US/09984130

Publication No. US20030055231A1

GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REFERENCE: PF489P2
CURRENT APPLICATION NUMBER: US/09/984,130
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,792
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 09/836,353
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR FILING DATE: 2000-04-19
PRIOR APPLICATION NUMBER: PCT/US99/25031
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR FILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 148
LENGTH: 2338
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (3)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (6)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (9)
OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (32)

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US-09-978-295A-258
Sequence 258, Application US/09978295A
Patent No. US20020156006A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: P263P1C11

CURRENT APPLICATION NUMBER: US/09/978,295A

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364

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PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392

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RESULT 11

US-09-978-697-258

Sequence 258, Application US/09378697

Patent No. US20020169284A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
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APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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/ PRIOR APPLICATION NUMBER: 60/085697

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RESULT 12

US-09-978-192A-258
; Sequence 258, Application US/09978192A
; Patent No. US20020177553A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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[illegible]

APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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APPLICANT: Gurney, Austin L.
APPLICANT: Hillen, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuc, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918595
PRIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559

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Db 946 CTGGAAGAACTTGGGAACGCGAGTCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCGTC 1005
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Db 1621 CCTGAGGCCCCGATGCCCAAGGGCACCCAGCGGATTTATGCAAGTCAAGTTCCAA 1677
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; Sequence 258, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Klijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 258
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-608A-258
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Best Local Similarity 85.0%; Pred.No. 0;
Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps 1;

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Search completed: November 9, 2004, 02:38:52
Job time : 1363.51 secs

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479	OV	ACTTCTCCAGAAAGGGTGTGAGGGACACAGAGACCGTCCGACTCGTGTGGCCCTATGCC	538	
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850	DB	CCAGATCTCTTGCTATCAGCATTTTCCATGACATGTATCAGTC-----CCAGACTTGC	903	
599	OV	AGGGAATGTCCATACCTTGGAGGCCAAAAAGGCGAGTTCCTCGGCTCCTCTGTGCTG	658	
904	DB	ATGAGATCTCTTACATCTTGAAGTTTCAGCAAGGCCAGTCTCTTCGCTCCTCTGTACTG	963	
659	OV	CTGACGACGACCCCTTGCCACACTGAGCTGGGTCTCTCGAAGACAGAGTCTCTCTCTCT	718	
964	DB	CTGACGACGACCCCTTGCTACTGAGCTGGGTCTTAGAGGACCAAGTCTCTTCTTGGT	1023	
719	OV	CCCATCCCTGGGGCCCTAGACCCCTGGGCTGGAGCTGCCGGGTGAAGCTGGGGATT	778	
1024	DB	CTAGCCCTGTGGGGTCCAGAACCCCTGGCACTAGAGCTGCCCTGGTGAAGCTGGGGACT	1083	
779	OV	CAGGCGCTACACTCTCGAGGGAGAACAGAGCTTGGCTCCGAGAGGGAGCCCTGGACC	838	
1084	DB	CTGACACTACTCTGCCAAGCAGAGAAATAGAGCTGGGTCCCGACCAATACCTCTGAC	1143	
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899	OV	TCCTGGAACACTTGGGAAACGGACGTCTTCCCACTACTGGAGGGCCAAAGCCTGTGCC	958	
1204	DB	TGTTGGAATCTCTCAGGAATGCCATCTCCCTCCCACTCTGGAGGGCCAAAGCCTGTGCC	1263	
959	OV	TGCTGTGTGTACACACAGACAGCCCGACAGCAGAGCTGAGCTGGACCCAGAGGGGACAGG	1018	
1264	DB	TAGTCTGTGTCACTATAGCAATCCCGCCAGCCAAATGTGAGTGGGTGGTGTACACAGA	1323	
1019	OV	TTCTGAGCCCTCTCCACGCTCTCAGACCCCGGGTCTCTGGAGCTGCCTCGGTTCAGATGG	1078	
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1079	OV	AGACGAGAGAGATTCACTGCGCAGCTCGGACCCGACTGGGTCTCCAGCAGTCTCTC	1138	
1384	DB	AACATGAAGAGAGAAATTCACCTGTGTGACAGAAACCCACTGGGTGCCCAGCGCATCTCTC	1443	
1139	OV	TCAGCCTCTCCGTGCACTACTCTCCCGAAGCTGCTGGGCCCTCTCTGCTCTCTGGAGGCTG	1198	
1444	DB	TGAGCCTCTCTGTGCACTACCGCCCGCAGATGTCCAGCCCTCTCTCTCTGGAGGCCA	1503	
1199	OV	AGGCTGTGCACTGAGCTGTCTCTCCAGGCCAGCCCGGCCCTCTCTCTGCGGTGTGTGGC	1258	
1504	DB	AGGCTGTGCACTGCAACTGTCTCTCCAGAGCCTGGCTTGCCTCCCTCTGCTGTGGCGGC	1563	
1259	OV	TTGGGAGGAGCTCTGGAGGGGAAACAGCAGGCCAGGACTCTCTCGAGGTCAACCCCGAGCT	1318	
1564	DB	TGGGGAGGGGCTCTGGAGGGGAAACAGCAATGCTCTCTCTTCAAGTCACTTTTCACT	1623	
1319	OV	CAGCCGGCCCTGGCCAAACAGCTCCTGAGCCTCCATGAGGGCTCAGCTCCGGGCTCA	1378	
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1379	OV	GGCTCCGCTGTGAGGCTGGAGCTCCATGGGGCCAGGTGATCCATCTCTCAGCTGC	1438	
1684	DB	GGCTCAGCTGTGAGTCTTGGAACCCATGTAGGCCACCACTCTGTCTCTCTCTCTCT	1743	
1439	OV	CAGATAAGAGGAGACTCATCTCTCAAGGCCATTTCCACGGAGCGTTTCTTGGGAATCGGCA	1498	

Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, F., Saito, R., Saito, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-3216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/
 Location/Qualifiers

1.3939

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 mol_type="mRNA"
 strain="C57BL/6J"
 db_xref="FANTOM DB:9830164H23"
 db_xref="taxon:10090"
 clone="9830164H23"
 sex="male"
 tissue="bone"
 clone_lib="RIKEN full-length enriched mouse cDNA library"
 dev_stage="adult"
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note="unlabeled protein product; putative weakly similar to SIALIC ACID-BINDING LECTIN [Homo sapiens] (SPTR|Q96RL6, evidence: FASTA, 61.6% ID, 84.6% length, match=17.9);
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 db_xref="GI:26331816"
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polyA_signal
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 note="putative"

polyA_site
 3939
 note="putative"

ORIGIN

Query Match 33.2%; Score 635.8; DB 3; Length 3939;
 Best Local Similarity 69.5%; Pred. No. 4.6e-148;
 Matches 979; Conservative 0; Mismatches 342; Indels 88; Gaps 5;

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 Db |CTAGTCCAGACTTGCATGAGATCTTACATCTGGAAGTTCAGCAAGCCAGTCTC 2330
 641 TGGGGTCTCTGCTGCTGAGCAGCCAGCCCTGACCTGACCTGAGCTGGTCTGCGA 700
 Db |TTGCTCTCTCTGCTGCTGAGCAGCCAGCCCTGACCTGAGCTGGTCTGAGG 2390
 701 ACAGAGTCTCTCTGCTGCTGAGCAGCCAGCCCTGAGCCCTGAGGCTGCGGCG 760
 Db |ACCAAGTCTCTCTGCTGCTGAGCAGCCAGCCCTGAGCCCTGAGGCTGCGGCT 2450
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 Db |GGGTGAAAGCTGGGAGCTTGGACACTACATCTGCAAGCAGAGATAGGCTGGGCTCC 2510

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 941 AGGGCAAAAGCTGTGCTGT 1000
 Db |AGGGCAAAAGCTGTGCTGT 2690
 1001 G3ACCCAGAGGGGACAGTCTCTGAGCCCTCTCCAGCCCTCAGACCCCGGGGTCTCTGGAGC 1060
 Db |GGGTGTGGT 2750
 1061 TGCCTCGGGTTCAGT 1120
 Db |TGCCTCGGGTTCAGT 2810
 1121 GCTCCACGACGCTCTCTGT 1156
 Db |GTGCCCCAGGCGATCTCTGT 2870
 1157 -----ACTCCCGAAGCTG 1170
 2871 GATCTGT 2930
 1171 CTGGGCGCTCTCTGT 1230
 Db |TCCAGCGCCCTCTCTGT 2990
 1231 AGCCCGGCGCCCTCTCTGT 1290
 Db |TGGCTGT 3050
 1291 CAGGACTCTTCAGAGT 1350
 Db |AATGCTCTTCAGAGT 3110
 1351 CTCATGT 1410
 Db |CTCTTCAGAGT 3170
 1411 GCCCAGAGT 1470
 Db |GCCCAGACCACTCTGT 3224
 1471 TCCACGAGGCTTCTGGGATCGGATCAGGCTCTTCTTTCTCTGTGTGTGTGTGTGTGTGTGT 1530
 Db |TCCAGGAGGAGT 3284
 1531 ATCATCATGAAGATTCTACCGAAGAGACGGACTCAGACAGAAACCCGAGGCGCCAGGTTC 1590
 Db |GTATCGTGAAGACCTCCAGAAAGAAAGAACCCAGAGGAACCTCCAGGCGCCAGGTTC 3344
 1591 TCCCGGACACGACAGTCTGT 1650
 Db |TCCCGGACACGACAGTCTGT 3404
 1651 CAGAAGCGGAATCAGAAGCCACCAACAGTCTCTGGACCCCTCTTCCACCAAGGTGCT 1710
 Db |CGAATGTGAAGCTGTGAACAGATGCCCCCTTCTAGAGCTCACCCCTCGACACT 3458
 1711 CCCTCCCGCAGAAATCAAGAAAGAACCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1767
 Db |CACCTCCCAACCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 3518
 1768 GAAACCAATCATCACTCAGAGCCCGCAGAAATCCAGAGAGCCAGAGGAGCTCCATAT 1827
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/db_xref="taxon:9606"
/clone="IMAGE958K041152 ; IMAGE:4297851"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 48"
/notes="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;
Site: 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."

ORIGIN
Query Match      26.3%; Score 505; DB 5; Length 505;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 841 TCTGTGAGTATCTCTCAGAGAACCTGAGAGTATGTTTCCCAAGCAACAGGACAGTC 900
DB 1 TCTGTGAGTATCTCTCAGAGAACCTGAGAGTATGTTTCCCAAGCAACAGGACAGTC 60

QY 901 CTGGAACCTTGGAGCGACAGTCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCTG 960
DB 61 CTGGAACCTTGGAGCGACAGTCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCTG 120

QY 961 GTCTGTGTACACACAGACGCCCCAGCCAGCGTGTGAGTGGACCCAGAGGGGACAGGTT 1020
DB 121 GTCTGTGTACACACAGACGCCCCAGCCAGCGTGTGAGTGGACCCAGAGGGGACAGGTT 180

QY 1021 CTGAGCCCTCCAGCCCTCAGACCCGGGTCTCTGAGTGGTCTGGTCTGAGTGGAG 1080
DB 181 CTGAGCCCTCCAGCCCTCAGACCCGGGTCTCTGAGTGGTCTGGTCTGAGTGGAG 240

QY 1081 CAGAGGAGAGTTTCACTCCACGCTGGCACCCACTGGGCTTCCAGACAGTCTCTCTC 1140
DB 241 CAGAGGAGAGTTTCACTCCACGCTGGCACCCACTGGGCTTCCAGACAGTCTCTCTC 300

QY 1141 AGCTTCTCTGACTACTCCCGAAGTCTCTGGGCCCCCTCTCTGCTCTGGAGGCTGAG 1200
DB 301 AGCTTCTCTGACTACTCCCGAAGTCTCTGGGCCCCCTCTCTGCTCTGGAGGCTGAG 360

QY 1201 GGTCTGACTGAGTCTCTCTCCAGGCCAGCCCGCCCCCTCTCTGGCTGGTGGCTT 1260
DB 361 GGTCTGACTGAGTCTCTCTCCAGGCCAGCCCGCCCCCTCTCTGGCTGGTGGCTT 420

QY 1261 GGGAGGAGTCTGGAGGGGAACAGCAGCCAGGACTCTTCGAGGTACCCCCAGCTCA 1320
DB 421 GGGAGGAGTCTGGAGGGGAACAGCAGCCAGGACTCTTCGAGGTACCCCCAGCTCA 480

QY 1321 GCCGGGCCCTGGGCCAACAGCTCCC 1345
DB 481 GCCGGGCCCTGGGCCAACAGCTCCC 505
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DEFINITION 17000424511003 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION  CN369197
VERSION    CN369197.1  GI:47369131
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 730)
AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
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Li,Y., Xu,C., Pang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 850 473 8658
Fax: 850 473 7760
Email: rbrandenberger@geron.com
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FEATURES

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H9"
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from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"
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ORIGIN

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Query Match      23.8%; Score 456.2; DB 7; Length 730;
Best Local Similarity 79.3%; Pred. No. 3.7e-103;
Matches 508; Conservative 0; Mismatches 118; Indels 41; Gaps 4;

QY 78 GGAGTCAGTATGTTGCGGAGGGGCTGTGCATCTCTGTGCCCTGCTTTCTCTACCC 137
DB 730 GGAGTCAGTATGTTGCGGAGGGGCTGTGCATCTCTGTGCCCTGCTTTCTCTACCC 671

QY 138 CGACACAGCTGGACAGGGTCTACCCAGCTTATGGCTACTGGTTCAAAGCAGTACTGA 197
DB 670 CGACACAGCTGGACAGGGTCTACCCAGCTTATGGCTACTGGTTCAAAGCAGTACTGA 611

QY 198 GACAAACCAAGGGTCTCTGTGGCCACAAACACACAGAGTCGAGGTGGAATGAGCAC 257
DB 610 GACAAACCAAGGGTCTCTGTGGCCACAAACACACAGAGTCGAGGTGGAATGAGCAC 551

QY 258 CCGGGGCGAGTCCAGCTCACTGGGGATCCGCCAAGGGAACTGCTCTCTTGGTATCAG 317
DB 550 CCGGGGCGAGTCCAGCTCACTGGGGATCCGCCAAGGGAACTGCTCTCTTGGTATCAG 491

QY 318 AGACCGCAGAGTGCAGGATGAGTCACAGTACTTCTTCGGGTGGAGAGGAAGTATGT 377
DB 490 AGACCGCAGAGTGCAGGATGAGTCACAGTACTTCTTCGGGTGGAGAGGAAGTATGT 431

QY 378 GAGATATATTTTCAAGCATGGGTCTTTCTTAAAGTAACAGTCTCAGTTTACGCC 437
DB 430 TGTGGACTTCTCCAGAAAGGGTG----- 408

QY 438 CAGACCCAGGACCAACACACAGCTCACCTGCGCATGTGGACTTCTCCAGAAAGGGT-G 496
DB 407 -TGAGCGCACAGAGACCGTCCGACTCGCTGTGGCTGTGAGTGTGGCTGGAGGGTGG 349

QY 497 TGAGCGCACAGAGGACCGTCCGACTTCCGTGTGGCCCTATGCCCGCCAGAGACCTTGTATCA 556
DB 348 GGTGTGCAGACAGCCCGGTGGGTGGGAGGTGGAGAGAGCCAGTGGGACAGTGGAGCGCG 289

QY 557 GCATTTTCAGTGA-CAACACCGCCAGCCCTGGAGCGCCAGCCAGGGAAATGTCCCATAC 615
DB 288 TCCCAGCTCAGGAGCATTCAGGGAGAGGAAGCTGTGGGGTCCCAGGATGCCCGCGAGCC 229

QY 616 CTGGAAGCCCAAAAGGCCAGTCTCTGCGGCTCTCTGTGTGTGTGTCGACAGCAGCCCT 675
DB 228 CTGGAAGCCCAAAAGGCCAGTCTCTGCGGCTCTCTGTGTGTGTGTCGACAGCAGCCCT 169

QY 676 GCACACTGAGTGGTCTCTGCAGAACAGAGTCTCTCTCGTCCCATCCCTGGGGCCCT 735
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121 TGCTCTTTCTCTACCCCGGACAAAGACTGGACAGGCTCTACCCAGCTTATGGCTACTGG 180
Db TGCTCTTTCTCTACCCCGGACAAAGACTGGACAGGCTCTACCCAGCTTATGGCTACTGG 242
Qy TTCAAGAGCTGACTGAGACAAACCAAGGCTCTCTGTGSCCAACCAACAGAGTCCA 240
Db TTCAAGAGCTGACTGAGACAAACCAAGGCTCTCTGTGSCCAACCAACAGAGTCCA 302
Qy GAGGTGGAATGAGCACCAGGCGGCGGATTCACAGCTCACTGGGATCCCGCCAGGGGAAC 300
Db GAGGTGGAATGAGCACCAGGCGGCGGATTCACAGCTCACTGGGATCCCGCCAGGGGAAC 362
Qy TGCTCTTTCTCTACCCCGGACAAAGACTGGACAGGCTCTACCCAGCTTATGGCTACTGG 360
Db TGCTCTTTCTCTACCCCGGACAAAGACTGGACAGGCTCTACCCAGCTTATGGCTACTGG 422
Qy GAGGTGGAATGAGCACCAGGCGGCGGATTCACAGCTCACTGGGATCCCGCCAGGGGAAC 420
Db GAGGTGGAATGAGCACCAGGCGGCGGATTCACAGCTCACTGGGATCCCGCCAGGGGAAC 482
Qy GTGCTGAGTTCAGGCC 437
Db GCCTGACTCAGAAGCC 499

RESULT 10
COS57070
LOCUS
DEFINITION
AGENCOURT_28539076 NIH_MGC_249 Rattus norvegicus cDNA clone
IMAGE:7376699 5', mRNA sequence.

ACCESSION
COS57070
VERSION
COS57070.1 GI:50369433
KEYWORDS
EST.
SOURCE
Rattus norvegicus (Norway rat)

ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 850)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cga@nci.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
DNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M15529 row: d column: 09
High quality sequence stop: 665.

FEATURES
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/clone="IMAGE:7376699"
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/clone_lib="NIH_MGC_249"
/note="Organ: spleen; Vector: pExpress-1; Site 1: EcoRV;
Site 2: NotI; RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (TRI-reagent method). cDNA
was primed using oligo-dt primer:
5'-pGACTGTTCTAGATCGGAGCGGCCGCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb
resulted in an average insert size of 1.4 kb. This primary

library is normalized (primary library is NIH_MGC_248)
and was constructed by Express Genomics (Frederick, MD).
Note: this is a NIH_MGC library"

ORIGIN
Query Match 21.6%; Score 413.8; DB 7; Length 850;
Best Local Similarity 77.1%; Pred. No. 1.7e-92;
Matches 516; Conservative 0; Mismatches 152; Indels 1; Gaps 1;

Qy 589 CCCAGCCCCAGGGAATGTCCCATACCTGGAAGCCCAAAAGGCCAGTTCCTCGGGTC 648
Db 16 CCAGAACTGAATAGGAATCCTTCACTCTGGAAGTTCAACAAGGCCAGTCTCTACGTC 75
Qy 649 CTCTGTGTCTGACAGCAGCCCTGCTCCACATCTGAGTGGTCTCTGCAACAGAGTC 708
Db 76 CTCTGTGTCTGACAGCAGCCCTGCTCCACATCTGAGTGGTCTCTGCAACAGAGTC 135
Qy 709 CTCTGTGTCTGACAGCAGCCCTGCTCCACATCTGAGTGGTCTCTGCAACAGAGTC 768
Db 136 CTCTGTGTCTGACAGCAGCCCTGCTCCACATCTGAGTGGTCTCTGCAACAGAGTC 195
Qy 769 GCTGGGATTTAGGGCGCTACACCTGCGAGCGGAGAACAGGCTTGGTCTCCAGCAGGA 828
Db 196 GCTGGGATTTAGGGCGCTACACCTGCGAGCGGAGAACAGGCTTGGTCTCCAGCAGGA 255
Qy 829 GCCTGAGCACTCTCTGTGAGTATCTCCAGAGAACCTGAGAGTGAATGTTTCCCAAGCA 888
Db 256 ACCCTGAGCACTCTCTGTGAGTATCTCCAGAGAACCTGAGAGTGAATGTTTCCCAAGCA 315
Qy 889 AACAGAGCACTCTGGAAGAACCTTGGGAAACCGGACAGTCTCTCCAGTACTGGAGGCCAA 948
Db 316 AACAGAGCACTCTGGAAGAACCTTGGGAAACCGGACAGTCTCTCCAGTACTGGAGGCCAA 375
Qy 949 AGCCTGTGCTGTCTGT 1008
Db 376 AGCCTGTGCTGT 435
Qy 1009 AGGCGAGAGGTTTCTGAGCCCTCTCCAGCCCTCAGACCCCGGGGTCTCTGAGTCTCG 1068
Db 436 GCGACACAGACCTGTATCCCAACCCAGTCTTCCAGAGCTGCTGGAGTGGTCTCTG 495
Qy 1069 GTTCAAGTGGAGCAGGAAGGAGTGTACCTGCCAGCTCGCACCCAGTGGTCTCCAG 1128
Db 496 GTTCAAGTGGAGCAGGAAGGAGTGTACCTGCCAGCTCGCACCCAGTGGTCTCCAG 555
Qy 1129 CACGTCTCTCAGGCTCTCGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1188
Db 556 CACGTCTCTCAGGCTCTCGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 615
Qy 1189 TGGAGGCTGAGGGTCTGCACTGCACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1248
Db 616 TGGAGGCTGAGGGTCTGCACTGCACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 674
Qy 1249 CGCTGGTGG 1257
Db 675 CGCTGGG 683

RESULT 11
BU696122
LOCUS
DEFINITION
LL2nl2696T7 Hematopoietic Stem Cell Subtracted Library Mus
musculus cDNA 5' similar to OB binding proteins, mRNA sequence.
ACCESSION
BU696122
VERSION
BU696122.1 GI:23604852
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 669)
REFERENCE
Phillips, R.L., Ernst, R.E., Brunk, B.P., Ivanova, N., Mahan, M.A.,
Deanehan, J.K., Moore, K.A., Overton, G.C. and Lemischka, I.R.

QY	62	TCTGGATACAGTGCAGGAGTCAGTATGG--TGCGGAGGCCCTGTGTCATCTCTGTGGCC	120
Db	93	ACAGTCTTCAAGTGCAGAGCCAGGTGCGCGNTGCCGAGGCCCTGTGTGCATCGTGTCT	152
QY	121	TGTCCTTTCTCTACCCCCGACAAGACTGGACAGGGTCTACCCAGCTATAGGCTACTGG	180
Db	153	TGCAACCTCTCCTACCCCGGGAATGGCTGGGACGAGTCTACTGCTGTATAGCTACTGG	212
QY	181	TTCAAAAGCAGTGCATGAGACAACCAAGGGTGTCTCTGTGGCCAACAACCAAGAGTCGA	240
Db	213	TTCAAAAGGACGACACGAGCCCAAGAACCGGTGCTCTGTGGCCATAACAACCAAGAGTCGA	272
QY	241	GAGGTGAAATGAGCACCCGGGGCCGATTTCAGGTCTACTGGGGATCCCGCCAAAGGGAAC	300
Db	273	GAGGTGAAATGAGCACCCGGGACCGGATTCAGGCTCACTGGGATCCCGCAAGGGAGC	332
QY	301	TGTCCTTGGTGATCAGAGACCGCGAGATGCAGATGATGATCAGTACTTCTTTCGGGTG	360
Db	333	TGTCCTTGGTGATCAGAGACCGCGAGAGGAGATGAGGCATGGTACTTCTTTCGGGTG	392
QY	361	GAGAGAGGAAGCTATGTGAGATATAATTTCATGAACGATGGTCTTCTTCTAAAGTAA--	418
Db	393	GAGAGAGGAAGCGGTGTGACATATAGTTTCTTGACCAATGCGTTCTTCTTAAAGTAAACA	452
QY	419	-----	418
Db	453	GCCTTGACTAAGAAAGCCTGATGTCTACATCCCGAGACCCCTGGAGCCCGGCGAGCCGGTG	512
QY	419	-----	418
Db	513	ACGGTCATCTGTGTGTTTAACTGGGGCTTTCAGAAATGTCCAGGCCCTTCTTTCTCTGG	572
QY	419	-----	426
Db	573	ACGGGGGTGCCTCTCCCTTAGAAGAACAGACCAAGCACCTCCACCTTCTCAGTGCCTC	632
QY	427	AGCTTACGCGCCAGACCCCGAGACCAACAACCGACCTCACCTGCCATGTGGACTTCTCC	486
Db	633	AGCTTACGCGCCAGACCCCGAGACCAACAACCGACCTCACCTGCCATGTGGACTTCTCC	692
QY	487	AGAAAGGGTGTGAGGCGCACAGAGGACCGTCCGACTCCGTGTGGCTATGCCCCACAGAC	546
Db	693	AGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGCTATG-CCCCAAGAC	751
QY	547	CTTGTTATCAGCATTTACGTGACAACAACGCCCGCCCTGGAGCCCGACCGCCAGGAAAT	606
Db	752	CTTATTATCAGCATTTTCAATCACAAACAGTCAGCCCTTGGAACT-----CCAGGGAAC	805
QY	607	GTCCCATACCTGGAAGCCCAAAAGGCCAGTTCTGTGGGCTCCCTGTGCTGTGTGACAGC	666
Db	806	GTCAATATCTGAGATTCAGAAAGCCAGTTCTGTGGCTTCTGTGTGTGTGTGACAGC	865
QY	667	CAGCCCCCTAGCCACTGAGCTGGGTCTGTGAGAACAGAGTCTCTCTCTGTCCCATCCC	726
Db	866	CAGCCCCCTGTGCMGCTGAGCTGGGTCTGTGAG-GCAGAGTCTTCTCTGTGTCCACCCC	924
QY	727	TGGGGCCCTAGACCCCTGGGGCTGAGCTGCCCGGGTGAAGGCTGGGGATTACAGGGCC	786
Db	925	TRGGGCMCMGAAACCTTGGGGTTCGARTCTGTGGGTACGGGGGGGGAATTAMGGGAC	984
QY	787	TACACTGCCGAG	799
Db	985	MCYTGCGASSGAG	997

SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 810)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin
CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1527 row: C column: 20
High quality sequence stop: 632.
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/clone_lib="NIH MGC 249"
/notes="Organ: spleen; Vector: pCpexpress-1; Site: 1: EcorV;
Site 2: NotI; RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (Tri-reagent method). cDNA
was primed using oligo-dT primer:
5'-pGACTGATTCATGCGAGCCGCCGCC (T)25-3' and cloned into
the EcorV/NotI sites of pCpexpress-1. Size-selection >1.25kb
resulted in an average insert size of 1.4 kb. This primary
library is normalized (primary library is NIH MGC 248)
and was constructed by Express Genomics (Frederick, MD).
Note: this is a NIH MGC library"

ORIGIN

Query Match	18.2%	Score 348;	DB 7;	Length 810;
Best Local Similarity	71.3%;	Pred. No. 5.4e-76;		
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Qy	1094	TCACCTGCCACGCTCGGCACCCCACTGGGTCC	CAGCAGCTCTCTCAGCGCTTCGGTGC	1153
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Qy	1154	ACTACTCCCCGAAGCTGTGGGCGCCTCTCTG	CTCTCTGGAGGCTGAGGGTCTGCACCTGCA	1213
Db	61	ACTACCCACCCAGATGTCAGACCCCTCTCTG	CTCTCTGGGATTCAGGGTCTGCACCTGCA	120
Qy	1214	GTTGCTCTCTCCAGGCGAGCCCGGCCCTCTC	TCCTGGCTGGTGGCTTGGGGAGAGCTGC	1273
Db	121	GCTGCTCTCCAGAGCCTGGGCTTGCCTCTCC	TGGGCTGGCGGCTGGGGAGGGGCTGC	180
Qy	1274	TGAGAGGGGAACAGCGCAGGAGTCTCTGAG	GTCAACCCCGCTCAGCGGGCCCTTGGG	1333
Db	181	TGAGGGGAACAGCAGCAATGCCTCTTCAG	GTCAACCTCCAGCTCACTTGGACCCCTGGG	240
Qy	1334	CCAACAGCTCCCTGAGCTCCATGAGGGGTCA	GCCTCCGCGCTCAGGCTCCGCTGTGAGG	1393
Db	241	CCAACAGCTCCCTGAGCTCCCTTCAGGAGTG	GGAACCCAGCCCTTGGCTCAGCTGTGAAG	300
Qy	1394	CTTGGAACGTCATGGGGCCCAAGTGGATTC	ATCTCTGAGCTGCCAGATAAGAGGGAC	1453
Db	301	CTTGGAACACCCATGGGGCCCAAGCACCCTC	TCCTCTGTGTGCTACTGATATAAAA	355

RESULT_13
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 LOCUS
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 DEFINITION
 IMAGE:7375918 5', mRNA sequence.
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 C0555499
 VERSION
 C0555499.1 GI:50367692
 KEYWORDS
 EST.

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ORIGIN			
Query Match		17.2%;	Score 329.8; DB 1; Length 580;
Best Local Similarity		75.0%;	Pred. No. 1.8e-71;
Matches 428;		Conservative 0;	Mismatches 137; Indels 6; Gaps 1;
QY	523	CGTGTGGCCTATGCCCGCAGAGACCTTGTTATCAGCATTTCACTGACACACAGCCAGCC	582
Db	16	CTTCTCCAGATGCCCGCAGATCTCTTGCTATCAGCATTTTCCATGACAAATGATCAGTC	75
QY	583	CTGGAGCCCCAGCCCGAGGGAATGCCCATACCTGGAAGCCCAAAAGGCCAGTTCCTG	642
Db	76	-----CCAGACTTGCATGAGAATCCTTCACATCTGGAAGTTCAGCAAGCCAGTCTCTT	129
QY	643	CGGTCCTCTGTGCTGTACAGCAGCCCGCTGCCACACTGAGCTGGGTCTTCGAGAAC	702
Db	130	CGCCTCTCTGTACTGTGTACAGCAGCGCCCTGCTACACTGAGCTGGGTCTTAGAGGAC	189
QY	703	AGAGTCCTCTCTGTCCTCCATCCCTGGGGCCCTAGACCCCTGGGGTGGAGCTGCCCGG	762
Db	190	CAAGTCCTTTCTTGGTCTAGCCCTGTGGGTGCGAAGCCCTGGCACTAGAGCTGCCCTGG	249
QY	763	GTGAAGGTGGGGAATTCAGGCGCTACACTGCGGAGCGGAGAACAGGCTTGGCTCCCG	822
Db	250	GTGAAGGTGGGGAATTCAGGCGCTACACTGCGGAGCGGAGAACAGGCTTGGCTCCCG	309
QY	823	CAGCAGCCCTGGACCTCTGTGCTGCTATCCTCCAGAGAACCTGAGAGTGATGGTTCC	882
Db	310	CAACATACCTTGGACCTCTGTGCTGCTATCCTCCAGAGAACCTGAGAGTGATGGTTCC	369
QY	883	CAAGCAAAACAGGACAGTCTTGAAAACTTTGGGAACGGCACGTCCTCTCCAGTACTGGAG	942
Db	370	CAAGCAAAACAGGACAGTCTTGAAAACTTTGGGAATGCCATCTCCCTCCAGTCTGGAG	429
QY	943	GGCCAAAGCCCTGTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1002
Db	430	GGCCAAAGCCCTGTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	489
QY	1003	ACCCAGAGGGGACAGGTTCTGAGCCCTCCAGCCCTCAGACCCCGGGGTCTTGGAGCTG	1062
Db	490	GCTTGGGTGACACAGACCCCTGATCCCAATCCAGTCTTCAGAGCCTGGGGTCTTGGAGCTG	549
QY	1063	CCTCGGGTTCAGTGGAGCAGGAGAGT	1093
Db	550	CCTCTGGTCCAGAGAGAACATGAAGAGAAAT	580

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1917	100.0	1917	3	AAA37848		Aaa37848 Human obe
2	1917	100.0	3099	2	AAV99912		Aav99912 Human sia
3	1917	100.0	3099	2	AAV99911		Aav99911 Human sia
4	1907.4	99.5	2295	3	AAa80610		Aaa80610 Human CD3
5	1907.4	99.5	2295	9	ADA27034		Ada27034 Human nov
6	1907.4	99.5	2295	12	ADBE86564		Adbe86564 Novel hum
7	1868	97.4	2954	6	ABK43361		Abk43361 DNA encod
8	1733	90.4	2208	6	ABK43367		Abk43367 DNA encod
9	1733	90.4	3024	6	ABK43373		Abk43373 DNA encod
10	1729.8	90.2	2176	12	ADI37009		Adi37009 Novel hum
11	1729.8	90.2	2176	12	ADL82804		Adl82804 Human PRO
12	1729.8	90.2	2338	9	ADA27152		Ada27152 Human nov
13	1721	89.8	3264	10	ADD19239		Add19239 Human cDN
14	1497.4	78.1	2823	6	ABK43362		Abk43362 DNA encod
15	1337	69.7	2565	6	ABK43360		Abk43360 DNA encod
16	1333.8	69.6	2764	2	AAz234109		Aaz234109 Human PRO
17	1333.8	69.6	2764	3	AAc78510		Aac78510 Human PRO
18	1333.8	69.6	2764	4	AAc45983		Aac45983 Human DNA
19	1333.8	69.6	2764	8	ACAc3677		Acac3677 Novel hum
20	1333.8	69.6	2764	8	ACA89433		AcA89433 cDNA encod
21	1333.8	69.6	2764	8	ACA73443		AcA73443 Human sec

181 TTCAAAGCAGTGAAGTCAAGCAACCAAGGGTGTCTCTGTGGCCACAAACACACAGAGTCGA 240
231 TTCAAAGCAGTGAAGTCAAGCAACCAAGGGTGTCTCTGTGGCCACAAACACACAGAGTCGA 290
241 GAGTGAAGTGAAGTCAAGCAACCAAGGGTGTCTCTGTGGCCACAAACACACAGAGTGA 300
291 GAGTGAAGTGAAGTCAAGCAACCAAGGGTGTCTCTGTGGCCACAAACACACAGAGTGA 350
301 TGCTCTGTGTGATCAGAGACGCGCAGATGACAGATGAGTCAAGTACATCTCTTGGGTG 360
351 TGCTCTGTGTGATCAGAGACGCGCAGATGACAGATGAGTCAAGTACATCTCTTGGGTG 410
361 GAGAGGAAGTGTGAGATATATTTTCAAGACGATGGGTCTCTTCTAAAGTAAACA 420
411 GAGAGGAAGTGTGAGATATATTTTCAAGACGATGGGTCTCTTCTAAAGTAAACA 470
421 GTGCTAGTTCAGGCTCAGAGACGCGCAGATGACAGATGAGTCAAGTACATCTCTTGGGTG 480
471 GTGCTAGTTCAGGCTCAGAGACGCGCAGATGACAGATGAGTCAAGTACATCTCTTGGGTG 530
481 TTCTCCAGGAAGGTGTGAGCAGCAGAGACGCTCGGCTCGGTGTGGCTATGCCCCC 540
531 TTCTCCAGGAAGGTGTGAGCAGCAGAGACGCTCGGCTCGGTGTGGCTATGCCCCC 590
541 AGAGACCTTGTATCAGCATTTTCAAGTGAACACACGCGCAGGCTGGAGCCCGACCCCGAG 600
591 AGAGACCTTGTATCAGCATTTTCAAGTGAACACACGCGCAGGCTGGAGCCCGACCCCGAG 650
601 GGAATGCTCCATACCTGGAAGCCCAAGAGGCGAGTTCCTGGGCTCTCTGTGCTGCT 660
651 GGAATGCTCCATACCTGGAAGCCCAAGAGGCGAGTTCCTGGGCTCTCTGTGCTGCT 710
661 GAGAGCAGCCCTGTCACACAGTGTGGGTCTGAGAACAGAGTCTCTCTCTGCTGTC 720
711 GAGAGCAGCCCTGTCACACAGTGTGGGTCTGAGAACAGAGTCTCTCTCTGCTGTC 770
721 CATCTCTGGGCTGAGACCTCTGGGCTGAGAGTCTGCGGGGTGAAGGTGGGATTC 780
771 CATCTCTGGGCTGAGACCTCTGGGCTGAGAGTCTGCGGGGTGAAGGTGGGATTC 830
781 GGGGCTTACACCTGCCAGCGGAGAACAGGCTTGGCTTCCAGCAGCGAGCCCTGGACCTC 840
831 GGGGCTTACACCTGCCAGCGGAGAACAGGCTTGGCTTCCAGCAGCGAGCCCTGGACCTC 890
841 TCTGTGAGTATCTCTCAGAGAACCTGAGAGTGTATGTTTCCCAAGCAACACAGACAGTC 900
891 TCTGTGAGTATCTCTCAGAGAACCTGAGAGTGTATGTTTCCCAAGCAACACAGACAGTC 950
901 CTGGAAGAACCTTGGAGACGCGAGTCTCTCCAGTACTGAGGGCCAGAGCTCTGCTG 960
951 CTGGAAGAACCTTGGAGACGCGAGTCTCTCCAGTACTGAGGGCCAGAGCTCTGCTG 1010
961 GTCTGTGTACACACAGCAGCCCGCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAGGTT 1020
1011 GTCTGTGTACACACAGCAGCCCGCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAGGTT 1070
1021 CTGAGCCCTCTCCAGCCCTCAGACCCCGGGGTCTGAGAGTGTCTGAGGTTCAAGTGGAG 1080
1071 CTGAGCCCTCTCCAGCCCTCAGACCCCGGGGTCTGAGAGTGTCTGAGGTTCAAGTGGAG 1130
1081 CACGAAGGAGTTCACCTGCGAGTCTGGACCCACTGGGCTCCAGCAGCTCTCTCTC 1140
1131 CACGAAGGAGTTCACCTGCGAGTCTGGACCCACTGGGCTCCAGCAGCTCTCTCTC 1190
1141 AGCTCTCTCGTGACTACTCCCCAGAGTCTGTTGGGCCCCCTCTCTCTCTGGAGGCTGAG 1200
1191 AGCTCTCTCGTGACTACTCCCCAGAGTCTGTTGGGCCCCCTCTCTCTCTGGAGGCTGAG 1250
1201 GGTCTGACCTGCACTGCTCTCTCCAGGCGAGCCCGCCCCCTCTCTCTGCGCTGCTGCTT 1260
1251 GGTCTGACCTGCACTGCTCTCTCCAGGCGAGCCCGCCCCCTCTCTCTGCGCTGCTGCTT 1310
1261 GGGAGGAGTGTGTGGAGGGGAAACAGCAGCCAGGACTCTCTTCGAGGTCAACCCCCAGCTCA 1320

1311 GGGGAGGAGTGTCTGGAGGGGAAACAGCAGCCAGGACTCTCTCGAGGTCAACCCAGCTCA 1370
1321 GCGGGCCCTCTGGGCGAAACAGCTCTCTGAGCTCTCATGAGAGGCTCAGTCTCGGCTCAGG 1380
1371 GCGGGCCCTCTGGGCGAAACAGCTCTCTGAGCTCTCATGAGAGGCTCAGTCTCGGCTCAGG 1430
1381 CTCCGCTGTGAGGCTGGAACGTCATGAGGCGCCAGAGTGGATCCATCTCTCAGCTGCA 1440
1431 CTCCGCTGTGAGGCTGGAACGTCATGAGGCGCCAGAGTGGATCCATCTCTCAGCTGCA 1490
1441 GATAAGAGGAGTCACTCAACGCGCATTTCTCAACGAGCGTCTTCTGGGAATCGGCATC 1500
1491 GATAAGAGGAGTCACTCAACGCGCATTTCTCAACGAGCGTCTTCTGGGAATCGGCATC 1550
1501 ACGGCTCTCTTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
1551 ACGGCTCTCTTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1610
1561 ACTCAGACAGAAACCCCGAGGCTCTCTCCGCGCACAGCAGATCCTTGATTTACATC 1620
1611 ACTCAGACAGAAACCCCGAGGCTCTCTCCGCGCACAGCAGATCCTTGATTTACATC 1670
1621 AATGTGTCCGACAGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
1671 AATGTGTCCGACAGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1730
1681 AGTCTCTCGACCCCTCTTCCACAGGCTCTCTCCGCGCACAGCAGATCCTTGATTTACATC 1740
1731 AGTCTCTCGACCCCTCTTCCACAGGCTCTCTCCGCGCACAGCAGATCCTTGATTTACATC 1790
1741 AAGCAGTATCAGTGTCCGAGTTCAGAAACCAAAATCATCTCAAGCCCGCAGATTC 1800
1791 AAGCAGTATCAGTGTCCGAGTTCAGAAACCAAAATCATCTCAAGCCCGCAGATTC 1850
1801 CAGGAGAGCCAGAGAGGCTCCATTTATCCAGCTCTCACTTCCGAGGCTCAGACCCAGG 1860
1851 CAGGAGAGCCAGAGAGGCTCCATTTATCCAGCTCTCACTTCCGAGGCTCAGACCCAGG 1910
1861 CTGAGGCGCGGATGCCCAAGCGCACCCAGCGGATTTATGAGAGTCAAGTTCCAA 1917
1911 CTGAGGCGCGGATGCCCAAGCGCACCCAGCGGATTTATGAGAGTCAAGTTCCAA 1967

RESULT 4

AAA80610

ID AAA80610 standard; cDNA; 2295 BP.

XX AAA80610;

XX AC

XX DT 21-NOV-2000 (first entry)

XX Human CD33-like secreted protein gene #5.

XX Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
XX antirheumatic; dermatological; antiproliferative; antiarteriosclerotic;
XX anticancer; vulnary; antiviral; antibacterial; antifungal;
XX immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
XX multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
XX Crohn's disease; nephritis; hyperproliferative disorder;
XX cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
XX melanoma; lymphoma; wound healing; human; ss.

XX Homo sapiens.

XX WC200029435-A1.

XX PD 25-MAY-2000.

XX XX 27-OCT-1999; 99WO-US025031.

XX PF 28-OCT-1998; 98US-0105971P.

XX XX

QY 1561 ACTGACAGAAACCCCGAGGCCAGGTTCTCCCGGCACAGCACGATCTGGATTACATC 1620
DB |||||
QY 1618 ACTGACAGAAACCCCGAGGCCAGGTTCTCCCGGCACAGCACGATCTGGATTACATC 1677
DB |||||
QY 1621 AATGTGGTCCCGACGGCTGCGCCCTGCTCAGAGCGGAATCAGAAAGCCACACCAAC 1680
DB |||||
QY 1678 AATGTGGTCCCGACGGCTGCGCCCTGCTCAGAGCGGAATCAGAAAGCCACACCAAC 1737
DB |||||
QY 1681 AGTCTCGAACCCCTCTTCCACAGAGTGTCTCCCTCCCGAGATCAAGAAAGAACAGAAA 1740
DB |||||
QY 1738 AGTCTCGAACCCCTCTTCCACAGAGTGTCTCCCTCCCGAGATCAAGAAAGAACAGAAA 1797
DB |||||
QY 1741 AAGCAGTATCAGTGTCCCGAGTTCAGAAACCAATCATCTCAAGCCGCCAGATCC 1800
DB |||||
QY 1798 AAGCAGTATCAGTGTCCCGAGTTCAGAAACCAATCATCTCAAGCCGCCAGATCC 1857
DB |||||
QY 1801 CAGGAGAGCAAGAGAGCTCCATTATGCGCAGGCTCAATCTCCAGGCTCAGACCCAGG 1860
DB |||||
QY 1858 CAGGAGAGCAAGAGAGCTCCATTATGCGCAGGCTCAATCTCCAGGCTCAGACCCAGG 1917
DB |||||
QY 1861 CTGAGGCGCGGATGCGCAAGGCCACCCAGCGGATATGCGAGAGTCAAGTCCAA 1917
DB |||||
QY 1918 CTGAGGCGCGGATGCGCAAGGCCACCCAGCGGATATGCGAGAGTCAAGTCCAA 1974
DB |||||

RESULT 5

AD227034
ID ADA27034 standard; cDNA; 2295 BP.

AC ADA27034;

DT 20-NOV-2003 (first entry)

DE Human novel secreted protein gene 5 cDNA HDPCL05 #1.

XX cytostatic; antiinflammatory; immunomodulator; neuroprotective;
KW homeostatic; gene therapy; cancer; inflammation; immune disorder;
KW neurological disorder; blood clotting disorder; food additive;
KW preservative; human; ss; secreted protein; gene.
XX Homo sapiens.

OS US200305231-A1.

PN 20-MAR-2003.

PD 29-OCT-2001; 2001US-00984130.

PF 28-OCT-1998; 98US-0105971P.

PR 27-OCT-1999; 99WO-US025031P.

PR 19-APR-2000; 2000US-0198407P.

PR 30-OCT-2000; 2000US-0243792P.

PR 18-APR-2001; 2001US-00836353.

XX (NIJ)/ NI J.

PA (YOUN)/ YOUNG P E.

PA (KENN)/ KENNY J J.

PA (OLSE)/ OLSEN H S.

PA (MOOR)/ MOORE P A.

PA (WEI)/ WEI Y.

PA (GREE)/ GREENE J M.

PA (RUBE)/ RUBEN S M.

PA (LIUD)/ LIU D.

PA (CROC)/ CROCKER P R.

XX Ni J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;

PI Ruben SM, Liu D, Crocker PR;

XX WPI; 2003-567103/53.

DR P-FSDB; ADA27052.

XX New human secreted nucleic acid molecules and polypeptides, useful for

PT

PT preventing, treating, or ameliorating a medical condition, such as
PT cancer, inflammation, immune disorders, neurological and blood clotting
PT disorders.

PS Claim 1; Fig 13; 454pp; English.

XX The invention relates to an isolated nucleic molecule that is at least
CC 95% identical to 18 human cDNA sequences representing 12 novel genes
CC encoding secreted proteins or a polynucleotide fragment of the cDNA
CC sequence contained in American Type Culture Collection (ATCC) deposit No.
CC defined in the specification, its species homologue, a variant or allelic
CC variant of the polynucleotide having a polynucleotide capable of
CC hybridising under conditions the polynucleotide, where the polynucleotide
CC does not hybridise under stringent conditions to a nucleic acid molecule
CC having a nucleotide sequence of only A or T residues. Also included are
CC recombinant vectors, host cells (for producing the polypeptide), the
CC secreted polypeptide (comprising a sequence that is at least 95%
CC identical to a polypeptide fragment, domain, epitope, full-length
CC protein, variant, allelic variant or species homologue), antibodies that
CC specifically bind to the polypeptides, diagnosing, treating, preventing
CC or ameliorating a medical condition by administering the polynucleotide
CC or the polypeptide, the gene corresponding to the cDNA sequence and
CC identifying an activity in a biological assay (by expressing the cDNA
CC sequence in a cell, isolating the supernatant, and detecting an activity
CC in a biological assay and identifying the protein in the supernatant
CC having the activity). The polypeptides, nucleic acids and antibodies are
CC useful for diagnosing a pathological condition or a susceptibility to a
CC pathological condition, for preventing, treating, or ameliorating a
CC medical condition, such as cancer, inflammation and other immune
CC disorders, neurological and blood clotting disorders (many examples are
CC given in the specification). The nucleic acids are also useful for
CC chromosome identification, radiation hybrid mapping or long-range
CC restriction mapping. The polypeptides and antibodies are useful for
CC providing immunological probes for differential identification of the
CC tissues immunohistochemistry assays. The polypeptide, polynucleotide,
CC agonist or antagonist may also be used as a food additive or preservative
CC to increase or decrease storage capabilities, fat content or other
CC nutritional components. The present is a secreted protein cDNA of the
CC invention.

XX Sequence 2295 BP; 494 A; 732 C; 620 G; 449 T; 0 U; 0 Other;

Query Match 99.5%; Score 1907.4; DB 9; Length 2295;

Best Local Similarity 99.7%; Pred. No. 0;
Matches 1911; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGCTACTGCCACTGCTGCTCTCTCGTGTGGCGGGTCCAGGCTATGATGGGAGA 60

DB 58 ATGCTACTGCCACTGCTGCTCTCGTGTGGCGGGTCCAGGCTATGATGGGAGA 117

QY 61 TTCTGGATACGAGTGCAGAGTCAAGTGTGTCGGAGGSCCTGTGCATCTCTTGCCC 120

DB 118 TTCTGGATACGAGTGCAGAGTCAAGTGTGTCGGAGGSCCTGTGCATCTCTTGCCC 177

QY 121 TGCTCTTTCTCTACCCCGCAAGACTGGACAGGCTTACCCAGCTTATGGCTACTGG 180

DB 178 TGCTCTTTCTCTACCCCGCAAGACTGGACAGGCTTACCCAGCTTATGGCTACTGG 237

QY 181 TTCAAAGCAGTCACTGAGACAAACCAAGGTCCTCTGTGGCCACAAACCCAGAGTGA 240

DB 238 TTCAAAGCAGTCACTGAGACAAACCAAGGTCCTCTGTGGCCACAAACCCAGAGTGA 297

QY 241 GAGGTGGAATGAGCACCAGGCGGCGGATTCAGCTCACTGGGGATCCGCCAAGGGGAAAC 300

DB 298 GAGGTGGAATGAGCACCAGGCGGCGGATTCAGCTCACTGGGGATCCGCCAAGGGGAAAC 357

QY 301 TGCTCTTTCTCTACCCCGCAAGACTGGACAGGTCCTCTGTGGCCACAAACCCAGAGTGA 360

DB 358 TGCTCTTTCTCTACCCCGCAAGACTGGACAGGTCCTCTGTGGCCACAAACCCAGAGTGA 417

QY 361 GAGAGAGAAGCTATGTGAGATATAATTTCTATGACGATGGTCTTTCTAAAGTACA 420

DB 418 GAGAGAGAAGCTATGTGAGATATAATTTCTATGACGATGGTCTTTCTAAAGTACA 477

421 GTGCTCAGCTTTCAGCCGACAGCCAGGACCAACACAGCACTCAGCTGCGATGTGGAC 480
 478 GTGCTCAGCTTTCAGCCGACAGCCAGGACCAACACAGCACTCAGCTGCGATGTGGAC 537
 481 TTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGGCTATGCCCC 540
 538 TTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGGCTATGCCCC 597
 541 AGAGACCTTGTATCAGCAATTTACGTGACAAACAGCCAGCCCTGAGAGCCGACAGCCAG 600
 598 AGAGACCTTGTATCAGCAATTTACGTGACAAACAGCCAGCCCTGAGAGCCGACAGCCAG 657
 601 GGAATGTCCCATACCTCGGAAGCCCAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCT 660
 658 GGAATGTCCCATACCTCGGAAGCCCAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCT 717
 661 GACAGCAGCCCTGCGCACTGAGTGGTCTGCGAAGCAGAGTCTCTCTCTCTCTCTCTCT 720
 718 GACAGCAGCCCTGCGCACTGAGTGGTCTGCGAAGCAGAGTCTCTCTCTCTCTCTCTCT 777
 721 CATCCCTGGGGCCCTAGACCCCTGGGCTGAGCTGCCGGGTGAAGCTGGGGATTCA 780
 778 CATCCCTGGGGCCCTAGACCCCTGGGCTGAGCTGCCGGGTGAAGCTGGGGATTCA 837
 781 GGGCGCTACACCTGCGGAGCGGAGAACAGGCTTGGCTCCAGCAGGAGCCCTGGACCTC 840
 838 GGGCGCTACACCTGCGGAGCGGAGAACAGGCTTGGCTCCAGCAGGAGCCCTGGACCTC 897
 841 TCTGTGAGTATCTCCAGAGAACCTGAGAGTGAATGGTTTCCCAAGCAACAGGACAGTC 900
 898 TCTGTGAGTATCTCCAGAGAACCTGAGAGTGAATGGTTTCCCAAGCAACAGGACAGTC 957
 901 CTGGAACACCTTGGGAACGCGACGTCTCTCCAGTACTGGAGGGCCAAAGCCCTGTGCTG 960
 958 CTGGAACACCTTGGGAACGCGACGTCTCTCCAGTACTGGAGGGCCAAAGCCCTGTGCTG 1017
 961 GTCTGTGTCAACACAGCAGCCCTCCAGCAGGCTGAGTGTGACCCAGAGGGGACAGGTT 1020
 1018 GTCTGTGTCAACACAGCAGCCCTCCAGCAGGCTGAGTGTGACCCAGAGGGGACAGGTT 1077
 1021 CTGAGCCCTCCAGCCCTCAGACCCCGGGTCTCTGAGCTGCTCGGTTCAAGTGGAG 1080
 1078 CTGAGCCCTCCAGCCCTCAGACCCCGGGTCTCTGAGCTGCTCGGTTCAAGTGGAG 1137
 1081 CAGAGGAGAGTTCACCTGCCAGCTCGGACCCCACTGGGCTCCAGCAGCTCTCTCTC 1140
 1138 CAGAGGAGAGTTCACCTGCCAGCTCGGACCCCACTGGGCTCCAGCAGCTCTCTCTC 1197
 1141 AGCTCTCCGTCAGTACTCCCGAAGCTGCTGGGCGCCCTCTGCTCTGGAGGCTGAG 1200
 1198 AGCTCTCCGTCAGTACTCCCGAAGCTGCTGGGCGCCCTCTGCTCTGGAGGCTGAG 1257
 1201 GGTCTGCACTGCACTGCTCTCTCCAGGCGAGCCCGGCCCTCTCTGCGCTGGTGGTT 1260
 1258 GGTCTGCACTGCACTGCTCTCTCCAGGCGAGCCCGGCCCTCTCTGCGCTGGTGGTT 1317
 1261 GGGGAGAGCTGTGAGGGGAAACAGCAGCAGGACTCTCTGAGTGTACCCCGAGCTCA 1320
 1318 GGGGAGAGCTGTGAGGGGAAACAGCAGCAGGACTCTCTGAGTGTACCCCGAGCTCA 1377
 1321 GCCGGGCTGGGCGCAACAGCTCCCTGAGCTCCATGGAGGCTCAGCTCCGGCTCAGG 1380
 1378 GCCGGGCTGGGCGCAACAGCTCCCTGAGCTCCATGGAGGCTCAGCTCCGGCTCAGG 1437
 1381 CTCGGCTGTGAGGCTGTGAGGAAAGCTGAGGCTGAGGCTGAGTGTGATCCATCTGAGTGGCA 1440
 1438 CTCGGCTGTGAGGCTGTGAGGAAAGCTGAGGCTGAGGCTGAGTGTGATCCATCTGAGTGGCA 1497
 1441 GATAAGAGGGACTCATCTCAAGCGGATTTCTCCAGCGAGCGTCTCTGGGAATCGGCATC 1500
 1498 GATAAGAGGGACTCATCTCAAGCGGATTTCTCCAGCGAGCGTCTCTGGGAATCGGCATC 1557

1501 ACGGCTCTCTTTTCTCTGCTGCTGCTGATCATCATGAAGATTCTACCGAAGAGCGG 1560
 1558 ACGGCTCTCTTTTCTCTGCTGCTGCTGATCATCATGAAGATTCTACCGAAGAGCGG 1617
 1561 ACTCAGACAGAAACCCCGAGGCCAGGTTCTCCCGGCACAGCAGGATCTCTGGATTACATC 1620
 1618 ACTCAGACAGAAACCCCGAGGCCAGGTTCTCCCGGCACAGCAGGATCTCTGGATTACATC 1677
 1621 AATGTGTCCCGACGCGTGGGCCCTCTGCTCAGAAAGCGGAATCAGAAAGCCACACCAAC 1680
 1678 AATGTGTCCCGAGCGGCTGGGCCCTCTGCTCAGAAAGCGGAATCAGAAAGCCACACCAAC 1737
 1681 AGTCTCTCGGACCCCTCTTCCACACGAGTCTCTCCCTCCCGAGATCAAGAAAGAACAGAAA 1740
 1738 AGTCTCTCGGACCCCTCTTCCACGAGTCTCTCCCTCCCGAGATCAAGAAAGAACAGAAA 1797
 1741 AAGCAGTATCAGTTGCCAGATTCCAGAACCCAAATCATCCACTCAAGGCCCGAGATCC 1800
 1798 AAGCAGTATCAGTTGCCAGATTCCAGAACCCAAATCATCCACTCAAGGCCCGAGATCC 1857
 1801 CAGGAGAGCCAGAGGAGCTCCATTATGCCACGCTCAACTTCCAGGCGTCAGACCCAGG 1860
 1858 CAGGAGAGCCAGAGGAGCTCCATTATGCCACGCTCAACTTCCAGGCGTCAGACCCAGG 1917
 1861 CTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGAGAAAGTCAAGTTCCAA 1917
 1918 CTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGAGAAAGTCAAGTTCCAA 1974

RESULT 6

ADE86564
 ID ADE86564 standard; cDNA; 2295 BP.
 AC ADE86564;
 XX AC ADE86564;
 DT 29-JAN-2004 (first entry)
 XX
 DE Novel human secreted protein cDNA #5.
 XX
 KW human; ss; gene; secreted protein; cancer; liver disorder; hepatitis;
 KW neural disorder; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN US2003129685-A1.
 XX
 PD 10-JUL-2003.
 XX
 PF 18-APR-2001; 2001US-00836353.
 XX
 PR 28-OCT-1998; 98US-0105971P.
 PR 27-OCT-1999; 99WO-US025031.
 PR 19-APR-2000; 2000US-0198407P.
 XX
 PA (NIJ)/ NI J.
 PA (YOUN)/ YOUNG P E.
 PA (Kenny)/ KENNY J J.
 PA (OLSE)/ OLSEN H S.
 PA (MOOR)/ MOORE P A.
 PA (WEIY)/ WEI Y.
 PA (GREE)/ GREENE J M.
 PA (RUBE)/ RUBEN S M.
 XX
 PI Ni J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;
 PI Ruben SM;
 XX
 DR WPI; 2004-020335/02.
 DR P-PSDB; ADE86582.
 XX
 PT New nucleic acid molecule, useful for preparing a medicament for
 PT preventing, treating or ameliorating a medical condition e.g. cancer,
 PT liver disorders or neural disorders.
 XX

1387	QY	TGTGAGGCTTGGAAAGTTCATCGGGGCCAGATGGATCCATCTCTCGAGCTGCCAGATAG	1446
1678	DB	TGTGAGGCTTGGAAAGTTCATCGGGGCCAGATGGATCCATCTCTCGAGCTGCCAGATAG	1737
1447	QY	AAGGAGACTCATCTCAACGSCATTCTCCAAAGCGAGCGTTTCTGGGAATCGGATCAACGGCT	1506
1738	DB	AAGGAGACTCATCTCAACGSCATTCTCCAAAGCGAGCGTTTCTGGGAATCGGATCAACGGCT	1797
1507	QY	CTTCTTTTCTCTGTGCTGTGCCCCGTGATCATCATGAAAGATTTCTACCGAAGAGAGCGACTCAG	1566
1798	DB	CTTCTTTTCTCTGTGCTGTGCCCCGTGATCATCATGAAAGATTTCTACCGAAGAGAGCGACTCAG	1857
1567	QY	ACAGAAACCCCGAGGCCAGGTTTCTCCGGGCACAGCAGCATCTCTGGATTACATCAATGTG	1626
1858	DB	ACAGAAACCCCGAGGCCAGGTTTCTCCGGGCACAGCAGCATCTCTGGATTACATCAATGTG	1917
1627	QY	GTCCGAGCGGTGGCCCCCTGTGCTCAGAAAGCGGAATCAGAAAGCCACACCAACAGTCTCT	1686
1918	DB	GTCCGAGCGGTGGCCCCCTGTGCTCAGAAAGCGGAATCAGAAAGCCACACCAACAGTCTCT	1977
1687	QY	CGGAGCCCTCTTTCACACGAGTGTCTCCCTTCCCAGAAATCAAAGAAAGAACCCAGAAAAGCAG	1746
1978	DB	CGGAGCCCTCTTTCACACGAGTGTCTCCCTTCCCAGAAATCAAAGAAAGAACCCAGAAAAGCAG	2037
1747	QY	TATCAGTTGCCAGTTTCCAGAACCCCAAAATCATCCATCAGGCCCCCAAGATCCCAAGAG	1806
2038	DB	TATCAGTTGCCAGTTTCCAGAACCCCAAAATCATCCATCAGGCCCCCAAGATCCCAAGAG	2097
1807	QY	AGCCAAAGGAGCTCCATTATTCGCAAGCTCAACTTCCCAGGCGTCAGACCCAGGCGCTCAG	1866
2098	DB	AGCCAAAGGAGCTCCATTATTCGCAAGCTCAACTTCCCAGGCGTCAGACCCAGGCGCTCAG	2157
1867	QY	GCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAAGTCAAGTTCCAA	1917
2158	DB	SCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAAGTCAAGTTCCAA	2208

ABK43373

AC
ABK43373:

XY
EY
ZNY

DE
DNA encoding sialic acid-binding Iq-related lectin, Siglec-BMS-L3-995-2.

Human; sialic acid-binding Ig-related lectin; SIGLEC; asthma;
immune system disease; leukaemia; allergy; inflammatory disease;
tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;
psoriasis; rheumatoid arthritis; conjunctivitis; cene; ss.

Homo sapiens.

OS Synthetic.

WO200208257-A2.

31-JAN-2002.

20-JUL-2001: 2001WO-US023082.

21-JUL-2000: 2000US-0220139P.

PA (BPTM) BRISTOL-MYERS SQUIBB CO.

PT Lonaphye M. Chang H. Whitney G:

WPT: 2002-241565/29

LA F-FGLB, FFA067067.
YY

IT
DT
NOVEL ISOLATED SINGLE
molecules useful for

Db 758 CTTGTTATCAGCAATTCACGTGACACACGCCAGCCCTCGAGCCCGCCAGCCCGAGGAAT 817
Qy 607 GTCCCATACCTGAAGCCCAAAAGCCAGTTCCTCGCGCTCCTCTGTCTCTGACAGC 666
Db 818 GTCCCATACCTGAAGCCCAAAAGCCAGTTCCTCGCGCTCCTCTGTCTCTGACAGC 877
Qy 667 CAGCCCGCTGACACCTGAGCTGGGTCCTGCAGAACAGAGTCTCTCTCTGCTCCATCC 726
Db 878 CAGCCCGCTGACACCTGAGCTGGGTCCTGCAGAACAGAGTCTCTCTCTGCTCCATCC 937
Qy 727 TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGTGAAGGCTGGGGATTCAGGGGCG 786
Db 938 TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGTGAAGGCTGGGGATTCAGGGGCG 997
Qy 787 TACACCTGCGAGCGAGAACAGGCTTGGCTCCACAGCGAGCCCTGACACTCTCTG 846
Db 998 TACACCTGCGAGCGAGAACAGGCTTGGCTCCACAGCGAGCCCTGACACTCTCTG 1057
Qy 847 CAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAAAGGACAGTCTGGAA 906
Db 1058 CAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAAAGGACAGTCTGGAA 1117
Qy 907 AACCTTGGGAACGCGACGCTCTCCAGTACTGAGAGGCGCAAGCCTGTGCTGTCTGT 966
Db 1118 AACCTTGGGAACGCGACGCTCTCCAGTACTGAGAGGCGCAAGCCTGTGCTGTCTGT 1177
Qy 967 GTCACACACAGCAGCCCGCCAGCCAGCTGAGCTGGACCCAGAGGGGACAGGTTCTGAGC 1026
Db 1178 GTCACACACAGCAGCCCGCCAGCCAGCTGAGCTGGACCCAGAGGGGACAGGTTCTGAGC 1237
Qy 1027 CCTCCAGCCCTCAGACCCCGGGGCTCTGAGCTGCTCGGTTCAAGTGAGACAGAA 1086
Db 1238 CCTCCAGCCCTCAGACCCCGGGGCTCTGAGCTGCTCGGTTCAAGTGAGACAGAA 1297
Qy 1087 GGAGAGTTACCTGCCAGCTCGGACCCACCTGGGCTCCAGACAGTCTCTCAGCCTC 1146
Db 1298 GGAGAGTTACCTGCCAGCTCGGACCCACCTGGGCTCCAGACAGTCTCTCAGCCTC 1357
Qy 1147 TCGGTGACCTACTCCCGAAGCTGTGCGGCCCTCTCTGCTCTGGAGGCTGAGGCTG 1206
Db 1358 TCGGTGACCTACTCCCGAAGCTGTGCGGCCCTCTCTGCTCTGGAGGCTGAGGCTG 1417
Qy 1207 CACTGAGCTGCTCTCCAGGCGCAGCCCGGCCCTCTCTGCTGCTGCTGCTGCTG 1266
Db 1418 CACTGAGCTGCTCTCCAGGCGCAGCCCGGCCCTCTCTGCTGCTGCTGCTGCTG 1477
Qy 1267 GAGCTGCTGAGGGGAACAGCAGCAGGACTCTCTGAGGTACCCCGCAGCTCAGCCGG 1326
Db 1478 GAGCTGCTGAGGGGAACAGCAGCAGGACTCTCTGAGGTACCCCGCAGCTCAGCCGG 1537
Qy 1327 CCTGGGCCAACAGCTCCCTGAGCTCCATGAGGGCTCAGCTCCGGCTCAGGCTCCGC 1386
Db 1538 CCTGGGCCAACAGCTCCCTGAGCTCCATGAGGGCTCAGCTCCGGCTCAGGCTCCGC 1597
Qy 1387 TGTGAGGCTGGAAGCTGCAATGGGCGCCAGAGTGGATCCATCTGCTGAGTCCAGATAAG 1446
Db 1598 TGTGAGGCTGGAAGCTGCAATGGGCGCCAGAGTGGATCCATCTGCTGAGTCCAGATAAG 1657
Qy 1447 AAGGAGCTCATCTCAACGGCATTTCTCAACAGGAGCGCTTTCTGGGAATCGGCATCAGCG 1506
Db 1658 AAGGAGCTCATCTCAACGGCATTTCTCAACGGAGCGCTTTCTGGGAATCGGCATCAGCG 1717
Qy 1507 CTTCTTTTCTCTGCTGCGCTGCTGATCATGATGATTCATGAGATTCATGAGATTCAG 1566
Db 1718 CTTCTTTTCTCTGCTGCGCTGCTGATCATGATGATTCATGAGATTCATGAGATTCAG 1777
Qy 1567 ACAGAAACCCCGAGGCGCGGTTCTCCCGGCACAGCAGTCTCTGATTCATCAATG 1626
Db 1778 ACAGAAACCCCGAGGCGCGGTTCTCCCGGCACAGCAGTCTCTGATTCATCAATG 1837
Qy 1627 GTCCCGAGCGCTGCGCCCTGCTGCTGAGAGCGGAATCAGAAAGCCACACCAACAGTCT 1686
Db 1838 GTCCCGAGCGCTGCGCCCTGCTGCTGAGAGCGGAATCAGAAAGCCACACCAACAGTCT 1897

Qy 1697 CGGACCCCTCTTCCACAGGTGCTCCCTCCCGAATCAAGAAAGAACCCAGAAAGCAG 1746
Db 1898 CGGACCCCTCTTCCACAGGTGCTCCCTCCCGAATCAAGAAAGAACCCAGAAAGCAG 1957
Qy 1747 TATCAGTTGCCAGTTTCCCGAAGAACCCAAATCATCTCAAGCCCGCCAGATCCAGGAG 1806
Db 1958 TATCAGTTGCCAGTTTCCCGAAGAACCCAAATCATCTCAAGCCCGCCAGATCCAGGAG 2017
Qy 1807 AGCAAGAGAGCTCCATATGCGACGCTCAACTTCCAGGCGTCAGACCCAGGCTGAG 1866
Db 2018 AGCAAGAGAGCTCCATATGCGACGCTCAACTTCCAGGCGTCAGACCCAGGCTGAG 2077
Qy 1867 GCCCGGATGCCCAAGGGCAGCCAGCGGATATGCAAGTCAAGTTCCAA 1917
Db 2078 GCCCGGATGCCCAAGGGCAGCCAGCGGATATGCAAGTCAAGTTCCAA 2128

RESULT 11
ADL82804

ID ADL82804 standard; cDNA; 2176 BP.

XX AC ADL82804;

XX DT 17-JUN-2004 (first entry)

XX Human PRO71236 cDNA, SEQ ID 6.

XX Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
XX Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
XX Gene Therapy; PRO; B cell related disorder; cancer;
XX immune-mediated inflammatory disease; human; gene; ss.

XX Homo sapiens.

XX WO2004024097-A2.

XX PD 25-MAR-2004.

XX PF 15-SEP-2003; 2003WO-US029097.

XX PR 16-SEP-2002; 2002US-0411392P.

XX (GETH) GENENTECH INC.

XX PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;

XX PI Wu TD;

XX WPI: 2004-329389/30.

XX P-PSDB; ADL82805.

XX New PRO polypeptide, useful for diagnosing and treating a B cell related
XX disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
XX mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.

XX Claim 2; Fig 6; 695pp; English.

XX The present invention relates to PRO proteins and their coding sequences.
XX The PRO proteins are useful for diagnosing and treating a B cell related
XX disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
XX antigen unresponsiveness, selective IgA deficiency, selective IgM
XX deficiency, selective deficiency of IgG subclasses, immunodeficiency with
XX hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
XX lymphoma, intermediate lymphoma, follicular lymphoma, type II
XX hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic
XX anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
XX ankylosing spondylitis. The PRO proteins are also useful for preparing a
XX medicament for treating a condition that is responsive to the PRO
XX protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
XX coding sequences are useful as hybridization probes in chromosome and
XX gene mapping, in preparing PRO proteins, or in generating transgenic
XX animals or knockout animals, which in turn are useful in the development
XX and screening of therapeutically useful reagents.

RESULT 12

ADA27152
ID ADA27152 standard: cDNA; 2338 BP.

ID ADA27152 standard; cDNA: 2338 bp.

AC ADA27152;

XX
XX

DT 20-NOV-2003 (first entry)
yy

Human novel secreted protein gene 5 cDNA HDPC1.05 #2

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KW cytostatic; antiinflammatory; immunomodulator; neuroprotective;

KW hemostatic; g

KW neurological dis

KW
yy
preservative

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 center

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CC
CCHH

PN US2003055231-A1.

XX

PD 20-MAR-2003.

[illegible]

PF 29-001-2001;
yy

28-OCT-1998: 981

PR 27-OCT-1999; 99W

PR 19-APR-2000; 2000U

PR 30-OCT-2000; 2000U

PR 18-APR-2001; 2001U

XX
DA /NYT TT / \ NYT T

PA (N100//) NI U.
PA (YOUN//) YOUNG P E

PA (KENN/) KENNY J J.

PA (OLSE//) OLSEN H S.

PA

PA (WEIY//) WEI Y.

PA (GREE//) GREENE J M.

PA (RUBE/) RUBEN S M.
PA (TUD/) LIT D

PA	(CROCK/)	CROCKER P R.
XX		
PI	NI J, Young PE, Kenny JU, Olsen HS, Moore PA, Wei Y, Greene JM;	
PI	Ruben SM, Liu D, Crocker PR;	
XX		
XX	WPI: 2003-567103/53.	
DR	P-PSDB; ADR27153.	
XX		
PT	New human secreted nucleic acid molecules and polypeptides, useful for	
PT	preventing, treating, or ameliorating a medical condition, such as	
PT	cancer, inflammation, immune disorders, neurological and blood clotting	
PT	disorders.	
PT		

PS Claim 1: Page 382-383: 454pp: English.

The invention relates to an isolated nucleic molecule that is at least 95% identical to 18 human cDNA sequences representing 12 novel genes encoding secreted proteins or a polynucleotide fragment of the cDNA sequence contained in American Type Culture Collection (ATCC) deposit No. 10000, defined in the specification, its species homologue, a variant or allelic variant of the polynucleotide having a polynucleotide capable of hybridizing under conditions the polynucleotide, where the polynucleotide does not hybridise under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A or T residues. Also included are recombinant vectors, host cells (for producing the polypeptide), the secreted polypeptide (comprising a sequence that is at least 95% identical to a polypeptide fragment, domain, epitope, full-length protein, variant, allelic variant or species homologue), antibodies that specifically bind to the polypeptides, diagnosing, treating, preventing or ameliorating a medical condition by administering the polynucleotide or the polypeptide, the gene corresponding to the cDNA sequence and identifying an activity in a biological assay (by expressing the cDNA sequence in a cell, isolating the supernatant, and detecting an activity

CC of the protein), preventing, treating or ameliorating a medical condition
CC by administering the nucleic acid or protein to a mammalian subject,
CC identifying a binding partner to the protein, the gene corresponding to
CC the cDNA sequence, and identifying an activity in a biological assay
CC (comprising expressing the nucleic acid in a cell, isolating the
CC supernatant, detecting an activity in a biological assay and identifying
CC the protein in the supernatant having the activity) The nucleic acids
CC and proteins display the following activities: Cytostatic, antibacterial,
CC Virucide, Neuroprotective, Gynaecological, Gastrointestinal-Gen,
CC Cardiant, Cardiovascular-Gen, Nephrotropic, Antiinflammatory, Muscular-
CC Gen, Respiratory-Gen, Immunosuppressive, Cerebroprotective, Vasotropic,
CC Nootropic, Antiallergic. The methods and compositions of the present
CC invention are useful for diagnosing, treating, preventing and/or
CC prognosticating disorders related to the novel polypeptides, such as
CC cancer, bacterial or viral infections, and neural, immune system, blood,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, inflammatory or proliferative disorders (many examples of these
CC diseases and disorders are given in the specification). The present
CC sequence encodes a novel secreted protein of the invention.

XX
SQ Sequence 3264 BP; 804 A; 965 C; 849 G; 646 T; 0 U; 0 Other;

Query Match 89.8%; Score 1721; DB 10; Length 3264;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1916; Conservative 0; Mismatches 0; Indels 175; Gaps 2;

QY 1 ATGCTACTGCCACGTCTGCTCTCTCTGCTGGCGGGTCCAGCGCTATGATGGGAGA 60
Db 43 ATGCTACTGCCACTGCTCTCTCTCTGCTGGCGGGTCCAGCGCTATGATGGGAGA 102
QY 61 TTCTGGATACGAGTCAGGAGTCAGTGATGGTCCGAGGGCTCTGTCATCTCTGTGCC 120
Db 103 TTCTGGATACGAGTCAGGAGTCAGTGATGGTCCGGA-GGCTGTGTCATCTCTGTGCC 161
QY 121 TGCCTCTTTCTCTACCCCGACAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGG 180
Db 162 TGCCTCTTTCTCTACCCCGACAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGG 221
QY 181 TTCAAAGCAGTGACTGAGACCAACCAAGGGTGCTCCTGTGGCCACAAACACAGAGTCGA 240
Db 222 TTCAAAGCAGTGACTGAGACCAACCAAGGGTGCTCTGTGCCACAAACACAGAGTCGA 281
QY 241 GAGGTGGAAATGAGCACCCGGGGCCGATTCAGCTCACTGGGATCCCGCAAGGGGAAC 300
Db 282 GAGGTGGAAATGAGCACCCGGGGCCGATTCAGCTCACTGGGATCCCGCAAGGGGAAC 341
QY 301 TGCCTCTGGTGATCAGAGACCGCAGATGCAGATCAGTCAAGTACTTCTTTGGGGTG 360
Db 342 TGCCTCTGGTGATCAGAGACCGCAGATGCAGATCAGTCAAGTACTTCTTTGGGGTG 401
QY 361 GAGAGAGGAAGCTATGTGAGATATAATTTCATGAACGATCGGTTCTTTCTAAAGTAA-- 418
Db 402 GAGAGAGGAAGCTATGTGAGATATAATTTCATGAACGATCGGTTCTTTCTAAAGTAA 461
QY 419 ----- 418
Db 462 GGCCTGACTCAGAACCTGATGTGTACATCCCGAGACCTGTGAGCGCCGGGCGACCGGGT 521
QY 419 ----- 418
Db 522 ACGGTCACTGTGTGTTTAACTGGGCCTTTGAGGAATGTCCACCCCTCTCTCTCTCTGG 581
QY 419 ----- 418
Db 582 ACGGGGGCTGCCCTCTCTCCCAAGAACCAACCAACGACCTCCCACTTCTCAGTGTCTC 641
QY 427 AGCTTCACGCCCCAGACCCCGAGACCACAAACACCGACCTCAGCTGCCATGTGGACTTCTCC 486
Db 642 AGCTTCACGCCCCAGACCCCGAGACCACAAACCGACCTCAGCTGCCATGTGGACTTCTCC 701
QY 487 AGAAAGGGTGTGAGCGCACAGAGGACCGTCCGATCCCGTGTGGCCTATGCCCCACAGAC 546
Db 702 AGAAAGGGTGTGAGCGCACAGAGACCGTCCGATCCCGTGTGGCCTATGCCCCACAGAC 761
QY 642 AGCTTCACGCCCCAGACCCCGAGACCACAAACCGACCTCAGCTGCCATGTGGACTTCTCC 701

QY	547	CTTGTTATCAGCATTTTCAGTGTACACACAGCCAGCCCTGGAGCCCCAGCCAGGGAAT	606
Db	762	CTTGTTATCAGCATTTTCAGTGTACACACAGCCAGCCCTGGAGCCCCAGGGAAT	821
QY	607	GTCCCATACCTGGAAGCCCAAAAAGGCCATTTCTCTCGGCTCTCTGTGTGTGTGACAGC	666
Db	822	GTCCCATACCTGGAAGCCCAAAAAGGCCATTTCTCTCGGCTCTCTGTGTGTGTGACAGC	881
QY	667	CAGCCCGCTGCCACATGAGCTGGGTCTTGCGAAGACAGAGTCTCTCTCTGTGTGTGTGAC	726
Db	882	CAGCCCGCTGCCACATGAGCTGGGTCTTGCGAAGACAGAGTCTCTCTCTGTGTGTGTGAC	941
QY	727	TGGGGCCCTAGACCCCTGGGGCTTGGAGCTGCCCGGGTGAAGCTCTGGGATTGAGGCGC	786
Db	942	TGGGGCCCTAGACCCCTGGGGCTTGGAGCTGCCCGGGTGAAGCTCTGGGATTGAGGCGC	1001
QY	787	TACACCTGCGGAGGAGACAGGCTTGCTCCAGCAGCGAGCCCTGGACCTCTCTGTG	846
Db	1002	TACACCTGCGGAGGAGACAGGCTTGCTCCAGCAGCGAGCCCTGGACCTCTCTGTG	1061
QY	847	CAGTATCTCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAACAGGACAGTCTTGAA	906
Db	1062	CAGTATCTCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAACAGGACAGTCTTGAA	1121
QY	907	AACCTTGGGAACGGCAGCTCTCTCCAGTACTTGGAGGGCCAGAGCCCTGCTGTCTGT	966
Db	1122	AACCTTGGGAACGGCAGCTCTCTCCAGTACTTGGAGGGCCAGAGCCCTGCTGTCTGT	1181
QY	967	GTCAACACAGCAGCCCCCAGCCAGGCTGAGCTTGAACCCAGAGGGACAGGTTCTGAGC	1026
Db	1182	GTCAACACAGCAGCCCCCAGCCAGGCTGAGCTTGAACCCAGAGGGACAGGTTCTGAGC	1241
QY	1027	CCCTCCCGGCCCTCAGACCCCGGGTCTTGAGAGCTGCCTCGGTTCAAGTGGAGCAGAA	1086
Db	1242	CCCTCCCGGCCCTCAGACCCCGGGTCTTGAGAGCTGCCTCGGTTCAAGTGGAGCAGAA	1301
QY	1087	GGAGAGTTACCTGCCACAGCTCGGCACCCACTGGGTTCCAGACAGTCTCTCTCAGCCTC	1146
Db	1302	GGAGAGTTACCTGCCACAGCTCGGCACCCACTGGGTTCCAGACAGTCTCTCTCAGCCTC	1361
QY	1147	TCGTCGATCTACCCGAGCTGCTGGGCCCTCTGCTCTCTGGAGGCTGAGGCTCTG	1206
Db	1362	TCGTCGATCTACCCGAGCTGCTGGGCCCTCTGCTCTCTGGAGGCTGAGGCTCTG	1421
QY	1207	CACCTGAGCTGTCTCTCCAGGCCAGCCCGGCCCTCTCTCGCTGTGTGGTGAGG	1266
Db	1422	CACCTGAGCTGTCTCTCCAGGCCAGCCCGGCCCTCTCTCGCTGTGTGGTGAGG	1481
QY	1267	GAGCTGCTGGAGGGACACAGCGAGGACTCTCTCGAGGTCACCCCAGCTCAGCCCGG	1326
Db	1482	GAGCTGCTGGAGGGACACAGCGAGGACTCTCTCGAGGTCACCCCAGCTCAGCCCGG	1541
QY	1327	CCCTGGGCCAACAGCTCTCCTGAGCTCCATGGAGGCTCAGCTCCGCGCTCAGGCTCCG	1386
Db	1542	CCCTGGGCCAACAGCTCTCCTGAGCTCCATGGAGGCTCAGCTCCGCGCTCAGGCTCCG	1601
QY	1387	TGTGAGGCTTGAAGCTTCCATGGGGCCAGAGTGGATCCATCTCTGAGCTGCCAGATAAG	1446
Db	1602	TGTGAGGCTTGAAGCTTCCATGGGGCCAGAGTGGATCCATCTCTGAGCTGCCAGATAAG	1661
QY	1447	AAGGGAATCATCTCAACGGCAATTTCTCCACGGAGCGTTCTTGGGAATCGGCATCACGGCT	1506
Db	1662	AAGGGAATCATCTCAACGGCAATTTCTCCACGGAGCGTTCTTGGGAATCGGCATCACGGCT	1721
QY	1507	CTTCTTTTCTCTGCTGCCCCGTATCATCATGAAGATTTCTACCGAAGAGACGGACTCAG	1566
Db	1722	CTTCTTTTCTCTGCTGCCCCGTATCATCATGAAGATTTCTACCGAAGAGACGGACTCAG	1781
QY	1567	ACAGAAACCCGAGGCCAGGTTCTCCCGCA CAGCAGATCTCTGGAAATCATCAATGTG	1626
Db	1782	ACAGAAACCCGAGGCCAGGTTCTCCCGCA CAGCAGATCTCTGGAAATCATCAATGTG	1841

1627 GTCCGACGGCTGCCCCCTGGCTCAGAGCGGAATCAGAAAGCCACCAACACAGTCCT 1686
 1842 GTCCGACGGCTGCCCCCTGGCTCAGAGCGGAATCAGAAAGCCACCAACACAGTCCT 1901
 1687 CGGACCCCTCTTCCACACAGGTGCTCCCTCCCAAGATCAAGAGGAGAACCAAGAGCAG 1746
 1902 CGGACCCCTCTTCCACACAGGTGCTCCCTCCCAAGATCAAGAGGAGAACCAAGAGCAG 1961
 1747 TATCAGTTGCCAGTTCCCGAGAACCAACCAATATCACTCAAGCCCGAGATCCAGGAG 1806
 1962 TATCAGTTGCCAGTTCCCGAGAACCAACCAATATCACTCAAGCCCGAGATCCAGGAG 2021
 1807 AGCCAAGAGGAGCTCCATTATGACACGCTCAACTTCCCGAGGCGTCAAGCCCGAGGCTGAG 1866
 2022 AGCCAAGAGGAGCTCCATTATGACACGCTCAACTTCCCGAGGCGTCAAGCCCGAGGCTGAG 2081
 1867 GCCCGGATGCCCAAGGCGACCCAGGCGGATTTATGAGAAGTCAAGTTCCAA 1917
 2082 GCCCGGATGCCCAAGGCGACCCAGGCGGATTTATGAGAAGTCAAGTTCCAA 2132

RESULT 14

ABK43362
 ID ABK43362 standard; cDNA; 2823 BP.

XX
 AC ABK43362;

XX
 DT 05-JUN-2002 (first entry)

XX
 DE DNA encoding sialic acid-binding Ig-related lectin, Siglec-BMS-L3c.

XX
 KW Human; sialic acid-binding Ig-related lectin; SIGLEC; asthma;
 KW immune system disease; leukaemia; allergy; inflammatory disease;
 KW tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;
 KW psoriasis; rheumatoid arthritis; conjunctivitis; gene; ss.

XX
 OS Homo sapiens.

XX
 PN WO200208257-A2.

XX
 ZB 31-JAN-2002.

XX
 EF 20-JUL-2001; 2001WO-US023082.

XX
 FR 21-JUL-2000; 2000US-0220139P.

XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX
 PI Longphre M, Chang H, Whitney G;

XX
 DR WPI; 2002-241565/29.

XX
 P-PSDB; AAU87076.

XX
 PT Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein
 PT molecules useful for treating immune system diseases such as asthma,
 PT leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.

XX
 PS Claim 11; Fig 4A; 209pp; English.

XX
 CC The invention relates to an isolated SIGLEC (sialic acid-binding Ig-
 CC related lectin) protein (I). Pharmaceutical compositions comprising (I)
 CC are useful for treating immune system diseases such as asthma, leukaemia
 CC or other allergic or inflammatory diseases. Extracellular domains of (I)
 CC represent potential markers for screening, diagnosis, prognosis, follow-
 CC up assays, and imaging methods. (I) is useful as a target for drugs which
 CC inhibit inflammation, tissue damage and remodeling in asthma, and
 CC inflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's
 CC disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is
 CC also useful for monitoring the course of disease or disorders, and for
 CC identifying agents that bind with and/or modulate the biological activity
 CC of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are
 CC useful in diagnosis and/or prognosis methods, and to detect the presence
 CC and/or amount of SIGLEC-BMS nucleotide sequences and/or SIGLEC-BMS

CC proteins in a biological sample. (II) are useful as nucleic acid probes
 CC are useful for screening genomic library to isolate a genomic clone of
 CC SIGLEC gene. SIGLEC-BMS gene copy number is determined for detecting
 CC diseases or disorders associated with SIGLEC-BMS transcripts or proteins.
 CC The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells
 CC expressing SIGLEC-BMS proteins and in diagnostic imaging technology.
 CC ABK43360-ABK43411 represent human SIGLEC coding sequences and PCR primers
 CC of the invention

XX
 SQ Sequence 2823 BP; 677 A; 855 C; 725 G; 566 T; 0 U; 0 Other;

Query Match 78.1%; Score 1497.4; DB 6; Length 2823;

Best Local Similarity 99.9%; Pred No. 0;

Matches 1498; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	419	CAGTCTCAGCTTCACGCCAGACCCAGAGACCAACACCGAGCTCACTGCGCATGTGG	478
DB	238	CAGTCTCAGCTTCACGCCAGACCCAGAGACCAACACCGAGCTCACTGCGCATGTGG	297
QY	479	ACTTCTCCAGAAAGGTGTGAGCGCACAGAGACCGTCCGACTCGTGTGCGCTATGCC	538
DB	298	ACTTCTCCAGAAAGGTGTGAGCGTACAGAGACCGTCCGACTCGTGTGCGCTATGCC	357
QY	539	CCAGAGACCTTTGTATCAGCATTTTACCGTGACACACCGAGCCCTGGAGCCCGAGCC	598
DB	358	CCAGAGACCTTTGTATCAGCATTTTACCGTGACACACCGAGCCCTGGAGCCCGAGCC	417
QY	599	AGGGAATGTCCCATACCTGGAGCCCAAAAGGCGAGTTCCTGCGCTCTCTGTGCTG	658
DB	418	AGGGAATGTCCCATACCTGGAGCCCAAAAGGCGAGTTCCTGCGCTCTCTGTGCTG	477
QY	659	CTGACAGCAGCCCGCTCCACACACTGAGCTGGGTCTCTGACAGACAGAGTCTCTCTCGT	718
DB	478	CTGACAGCAGCCCGCTCCACACACTGAGCTGGGTCTCTGACAGACAGAGTCTCTCTCGT	537
QY	719	CCCATCTCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAGGCTGGGATT	778
DB	538	CCCATCTCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAGGCTGGGATT	597
QY	779	CAGGCGCTACACCTCCGAGCGGAGAACAGGCTTGGCTCCACAGCAGGAGCCCTGGACC	838
DB	598	CAGGCGCTACACCTCCGAGCGGAGAACAGGCTTGGCTCCACAGCAGGAGCCCTGGACC	657
QY	839	TCTCTGTCAGTATCTCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAAAGAGCAG	898
DB	658	TCTCTGTCAGTATCTCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAAAGAGCAG	717
QY	899	TCCTGGAAACCTTGGGAAACGGACGCTCTCTCCAGTACTGGAGGGCCCAAGCCTGTGCC	958
DB	718	TCCTGGAAACCTTGGGAAACGGACGCTCTCTCCAGTACTGGAGGGCCCAAGCCTGTGCC	777
QY	959	TGGTCTGTGTACACACAGCAGCCCGCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAGG	1018
DB	778	TGGTCTGTGTACACACAGCAGCCCGCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAGG	837
QY	1019	TCTGAGCCCTCTCCAGCCCTCAGACCCCGGGTCTCTGAGAGTCCCTGCGTTCAAGTGG	1078
DB	838	TCTGAGCCCTCTCCAGCCCTCAGACCCCGGGTCTCTGAGAGTCCCTGCGTTCAAGTGG	897
QY	1079	AGCAGAGGAGAGTTTACCTCCGACCGCTCCGACCCACCACTGGGCTCCAGCAGCTCTCTC	1138
DB	898	AGCAGAGGAGAGTTTACCTCCGACCGCTCCGACCCACCACTGGGCTCCAGCAGCTCTCTC	957
QY	1139	TCAGCTCTCCGTCAGTACTCTCCCGAAGTGTCTGGGCGCCCTCTCTGCTCTGGAGGCTG	1198
DB	958	TCAGCTCTCCGTCAGTACTCTCCCGAAGTGTCTGGGCGCCCTCTCTGCTCTGGAGGCTG	1017
QY	1199	AGGCTCTGACCTGAGCTGTCTCTCCAGGCGACCGCGGCCCTCTCTGCGTGTGGTGGC	1258
DB	1018	AGGCTCTGACCTGAGCTGTCTCTCCAGGCGACCGCGGCCCTCTCTGCGTGTGGTGGC	1077
QY	1259	TGCGGAGAGAGTCTCTGGAGGGGAAACAGCAGCAGGACTCTCTGAGGTCAACCCAGCT	1318

541 AGAGACCTTGTATCAGCATTTACAGTGAACAACAGCCAGCCCTGGAGCCCCCAGCCCCAG 600
1523
669 AGAGACCTTGTATCAGCATTTACAGTGAACAACAGCCAGCCCTGGAGCCCCCAGCCCCAG 728
1740
601 GGAATCTCCATACCTGGAGCCCAAAAGGCGAGTTCCTGGGCTCCCTCTGTGTGCT 660
1583
729 GGAATGTCCCATACCTGGAGCCCAAAAGGCGAGTTCCTGGGCTCCCTCTGTGTGCT 788
1800
661 GACAGCAGCCCTGGCCACACTGAGCTGGTCTCTGAGAACAGAGTCTCTCTCTGTCTC 720
1643
789 GACAGCAGCCCTGGCCACACTGAGCTGGTCTCTGAGAACAGAGTCTCTCTCTGTCTC 848
1860
721 CATCCCTGGGCTTACAGCCTGGGCTGGAGTTCCTGGGCTGGAGTTCCTGGGCTGGAGTTC 780
1703
849 CATCCCTGGGCTTACAGCCTGGGCTGGAGTTCCTGGGCTGGAGTTCCTGGGCTGGAGTTC 908
1917
781 GGGGCTTACACTCCAGAGCGGAGAACAGGCTTGGCTCCAGAGCGAGCCCTGGAGCTTC 840
1760
909 GGGGCTTACACTCCAGAGCGGAGAACAGGCTTGGCTCCAGAGCGAGCCCTGGAGCTTC 968
1860
841 TCTGTGAGTATCTCCAGAGAACCTGAGAGTGTATGTTTCCAGAGAACAGAGCAAGTC 900
1917
969 TCTGTGAGTATCTCCAGAGAACCTGAGAGTGTATGTTTCCAGAGAACAGAGCAAGTC 1028
1917
901 CTGGAAACCTTGGGAAACGCGACCTCTCTCCAGTACTGGAGGCGCAAGGCTGTGCTG 960
1760
1029 CTGGAAACCTTGGGAAACGCGACCTCTCTCCAGTACTGGAGGCGCAAGGCTGTGCTG 1088
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961 GTCTGTGTACACAGAGCCCTCCAGAGCGGAGTGTAGTGTGAGTGTGAGTGTGAGTGTG 1020
1760
1089 GTCTGTGTACACAGAGCCCTCCAGAGCGGAGTGTAGTGTGAGTGTGAGTGTGAGTGTG 1148
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1021 CTGAGCCCTCCAGAGCGGAGTGTAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1080
1760
1149 CTGAGCCCTCCAGAGCGGAGTGTAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1208
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1081 CACGAAGGAGAGTTCAGCTGCGAGCTCGGAGCCCTCCAGAGCGGAGTGTGAGTGTGAGTGTG 1140
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1209 CACGAAGGAGAGTTCAGCTGCGAGCTCGGAGCCCTCCAGAGCGGAGTGTGAGTGTGAGTGTG 1268
1917
1141 AGCTCTCCGAGTACTCTCCAGAGCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1200
1760
1269 AGCTCTCCGAGTACTCTCCAGAGCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1284
1917
1201 GGTCTGCACTGAGTGTCTCTCCAGAGCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1260
1760
1285 ----- 1284
1261 GGGAGGAGTGTGAGAGGAGAACAGAGCCAGGAGTCTCTTGGAGTTCACCCAGCTCA 1320
1917
1285 ----- 1284
1321 GCCGGGCTGGGCAACAGTCTCTGAGCTTCAATGGAGGCTCAGTCTCGGCTCAGG 1380
1917
1285 ----- 1284
1381 CTCGGCTGTGAGGCTGGAAGTCTCATGGGCGGAGAGTGGATCCATCTCTCAGTGGCA 1440
1917
1285 ----- 1284
1441 GATGAAGGAGTCTCATGAGGAGTCTCAACGGAGGTTCTTGGGATCGGCATC 1500
1917
1285 -ATAAGAGGAGTCTCATGAGGAGTCTCAACGGAGGTTCTTGGGATCGGCATC 1343
1917
1501 ACGGCTCTCTTTTCTCTGCTGGGCTGATCATCATGAGATTTCTACCGAAGAGAGCG 1560
1917
1344 ACGGCTCTCTTTTCTCTGCTGGGCTGATCATCATGAGATTTCTACCGAAGAGAGCG 1403
1917
1561 ACTCAGACAGAAACCCGAGGCTGAGTCTCCGGGAGAGAGTCTCTGGATTTACATC 1620
1917
1404 ACTCAGACAGAAACCCGAGGCTGAGTCTCCGGGAGAGAGTCTCTGGATTTACATC 1463
1917
1621 AATGTGTCCGAGGCTGGGCTCTGGCTCAGAGCGGAGTATGAGAGGCGCACACCAAC 1680
1917

Search completed: November 8, 2004, 09:33:29
Job time : 1333.86 secs

1464 AATGTGTCCGAGCGCTGGCCCTCTGGCTCAGAGCGGAGTATGAGAGGCGCACACCAAC 1523
1917
1681 AGTCTCTCGAGCCCTCTTCCAGAGGCTCTCTCCAGAGTATCAAGAGGAGAGAGAGAG 1740
1917
1524 AGTCTCTCGAGCCCTCTTCCAGAGGCTCTCTCCAGAGTATCAAGAGGAGAGAGAGAG 1583
1917
1741 AAGCAGTATCAGTTCGAGGCTTCCAGAGGCTCTCTCCAGAGTATCAAGAGGAGAGAGAG 1800
1917
1584 AAGCAGTATCAGTTCGAGGCTTCCAGAGGCTCTCTCCAGAGTATCAAGAGGAGAGAGAG 1643
1917
1801 CAGGAGAGCGGAGAGGAGTCTCTATTCAGAGGCTCTCTCCAGAGGCTCTCAGAGGAGG 1860
1917
1644 CAGGAGAGCGGAGAGGAGTCTCTATTCAGAGGCTCTCTCCAGAGGCTCTCAGAGGAGG 1703
1917
1861 CTTGAGGCGGAGTCCCAAGGAGGCTCTCTCCAGAGGAGTATGAGAGGAGTCAAGTTCAG 1917
1917
1704 CTTGAGGCGGAGTCCCAAGGAGGCTCTCTCCAGAGGAGTATGAGAGGAGTCAAGTTCAG 1760
1917

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OM protein - protein search, using sw model

Run on: November 5, 2004, 13:50:18 ; Search time 112.542 Seconds
(without alignments)
2617.614 Million cell updates/sec

Title: US-09-937-636-3
Perfect score: 2706
Sequence: 1 MLPLILLSLLGGSQMDGR.....RPEARMPKGTQADYAEVRFQ 512

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2576.5	95.2	697	1	SILA_HUMAN
2	2265	83.7	544	2	Q6UXI8
3	2265	83.7	544	2	QAO88703
4	2185	80.7	425	2	BAC85493
5	1513.5	55.9	686	1	SILB_HUMAN
6	1343.5	49.6	688	2	Q80ZE3
7	1211.5	44.8	623	2	Q8BYI8
8	955	35.3	499	2	Q7Z728
9	947	35.0	499	1	SILB_HUMAN
10	909	33.6	595	1	SILL_HUMAN
11	909	33.6	597	1	SILL_PANTR
12	878	32.4	468	2	Q6PJ50
13	878	32.4	468	2	AQY9834
14	878	32.4	468	2	AAQ72479
15	878	32.4	468	2	AAH23280
16	873	32.3	467	1	SILS_MOUSE
17	870	32.2	463	1	SILY_MOUSE
18	861	31.8	439	2	Q6GTU4
19	836	30.9	442	1	SIL6_HUMAN
20	832.5	30.8	467	1	SILL_HUMAN
21	804.5	29.7	551	1	SIL5_HUMAN
22	796.5	29.4	551	2	AAH29896
23	792	29.3	394	2	Q6UXG0
24	792	29.3	394	2	AAQ88735
25	787	29.1	437	2	AAH35359
26	698	25.8	364	2	CAD36503
27	694	25.6	364	1	CD33_HUMAN
28	689.5	25.5	569	1	SILF_MOUSE
29	664	24.5	269	2	Q8BTG2
30	625	23.1	523	2	Q80ZE2
31	530.5	19.6	304	2	Q8Iw38

32	529	19.5	233	2	AAS89010
33	528	19.5	233	2	AAS89009
34	528	19.5	403	1	CD33_MOUSE
35	525	19.4	233	2	AAS89008
36	514	19.0	233	2	AAS89011
37	471.5	17.4	423	2	Q8BU57
38	454.5	16.8	293	2	BAC27845
39	371.5	13.7	287	2	Q9P0F8
40	362.5	13.4	237	2	AAO26206
41	360.5	13.3	269	2	Q9SKP9
42	358.5	13.2	271	2	Q9SKQ0
43	351.5	13.0	269	2	Q95KP8
44	303.5	11.2	626	1	MAG_HUMAN
45	302.5	11.2	620	1	SMP_COTVA

ALIGNMENTS

RESULT 1

ID	SILA_HUMAN	STANDARD;	PRT;	697 AA.
AC	Q96LC7; Q96G54; Q96LC8;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Sialic acid binding Ig-like lectin 10 precursor (Siglec-10) (Siglec-like protein 2).			
GN	Name=SIGLEC10; Synonyms=SLG2;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_taxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RX	MEDLINE=21303047; PubMed=11409878; DOI=10.1006/bbrc.2001.5053;			
RA	Yousef G.M., Ordon M.H., Fousias G., Diamandis E.P.;			
RT	"Molecular characterization, tissue expression, and mapping of a novel Siglec-like gene (SLG2) with three splice variants.";			
RL	Biochem. Biophys. Res. Commun. 284:900-910(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Spleen;			
RA	Munday J., Kerr S., Ni J., Cornish A.L., Zhang J.Q., Nicoll G.,			
RT	Floyd H., Mattei M.-G., Moore P., Liu D., Crocker P.R.;			
RT	"Identification, characterization and leucocyte expression of Siglec-10, a novel human sialic acid-binding receptor.";			
RL	Biochem. J. 355:489-497(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	TISSUE=Dendritic cell;			
RA	Li N., Zhang W., Wan T., Zhang J., Chen T., Yu Y., Wang J., Cao X.;			
RT	"Cloning and characterization of Siglec-10, a novel sialic acid binding member of the Ig superfamily, from human dendritic cells.";			
RL	J. Biol. Chem. 276:28106-28112(2001).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 3), ALTERNATIVE SPLICING (ISOFORMS 4 AND 5), MUTAGENESIS OF TYR-667, AND INTERACTION WITH PTPN6.			
RX	MEDLINE=21359381; PubMed=11358961; DOI=10.1074/jbc.M100467200;			
RA	Kitzig F., Martinez-Barriocanal A., Lopez-Botet M., Sayos J.;			
RT	"Cloning of two new splice variants of Siglec-10 and mapping of the interaction between Siglec-10 and SHP-1.";			
RL	Biochem. Biophys. Res. Commun. 296:355-362(2002).			
RN	[5]			
RP	SEQUENCE OF 337-697 FROM N.A. (ISOFORM 1/3/4).			
RC	TISSUE=B-cell;			
RX	MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,			

Aas89010	pan trogl
Aas89009	pan panis
Qc3994	mus musculu
Aas89008	gorilla g
Aas89011	homo sapi
Q8bu57	mus musculu
Bac27845	mus muscu
Q9p0f8	homo sapien
Aac26206	homo espi
Q9skp9	gorilla gor
Q9skq0	pan paniscu
Q95kp8	pongo pygma
P20916	homo sapien
Q21514	coturnix co

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Joquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blackley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 CC -!- FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. Preferentially binds to alpha2,3- or 2,6-linked sialic acid. The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell surface. In the immune response, may act as an inhibitory receptor upon ligand induced tyrosine phosphorylation by recruiting cytoplasmic phosphatase(s) via their SH2 domain(s) that block signal transduction through dephosphorylation of signaling molecules.
 CC -!- SUBUNIT: Interacts with PTPN6/SHP-1 upon phosphorylation.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1-4); secreted (isoform 5).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=5;
 CC Name=1; Synonyms=Long;
 CC IsoId=Q961C7-1; Sequence=Displayed;
 CC Name=2; Synonyms=Short, Sv1;
 CC IsoId=Q961C7-2; Sequence=VSP_002565;
 CC Name=3; Synonyms=SV3;
 CC IsoId=Q961C7-3; Sequence=VSP_002564;
 CC Name=4; Synonyms=SV4;
 CC IsoId=Q961C7-4; Sequence=VSP_002561;
 CC Name=5; Synonyms=SV2;
 CC IsoId=Q961C7-5; Sequence=VSP_002562;
 CC -!- TISSUE SPECIFICITY: Expressed by peripheral blood leukocytes (eosinophils, monocytes and a natural killer cell subpopulation). Isoform 5 is found to be the most abundant isoform. Found in lymph node, lung, ovary and appendix. Isoform 1 is found at high levels and isoform 2 at lower levels in bone marrow, spleen and spinal chord. Isoform 2 is also found in brain. Isoform 4 is specifically found in natural killer cells.
 CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in modulation of cellular responses. The phosphorylated ITIM motif can bind the SH2 domain of several SH2-containing phosphatases.
 CC -!- PTM: Phosphorylation of Tyr-667 is involved in binding to PTPN6.
 CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (sialic acid binding Ig-like lectin) family.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 CC ENBL; AY029277; AAK40255.1; -
 CC ENBL; AY029277; AAK40256.1; -
 CC ENBL; AF310233; AAK55139.1; -
 CC ENBL; AF311905; AAK92542.1; -
 CC ENBL; AY032485; AAK51124.1; -
 CC ENBL; BC009955; AAK09955.2; -
 CC HSSP; Q9Y286; 107S.

DR Genew: HGNC:15620; SIGLEC10.
 DR MIM: 606091; -
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00408; IGC2; 2.
 DR PROSITE: PS00835; IG LIKE; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Alternative splicing; Cell adhesion; Glycoprotein;
 KW Immunoglobulin domain; Lectin; Phosphorylation; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 16 Potential.
 FT CHAIN 17 697 Sialic acid binding Ig-like lectin 10.
 FT DOMAIN 17 550 Extracellular (Potential).
 FT TRANSMEM 551 571 Potential.
 FT DOMAIN 572 697 Cytoplasmic (Potential).
 FT DOMAIN 18 121 Ig-like V-type.
 FT DOMAIN 146 231 Ig-like C2-type 1.
 FT DOMAIN 251 339 Ig-like C2-type 2.
 FT DOMAIN 344 441 Ig-like C2-type 3.
 FT SITE 595 600 ITIM motif 1.
 FT SITE 665 670 ITIM motif 2.
 FT DISULFID 36 173 By similarity.
 FT DISULFID 41 101 By similarity.
 FT DISULFID 164 215 By similarity.
 FT DISULFID 276 323 By similarity.
 FT DISULFID 380 425 By similarity.
 FT MOD_RES 667 667 Phosphotyrosine.
 FT CARBOHYD 100 100 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 355 355 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 364 364 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 486 486 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 504 504 N-linked (GlcNAc...) (Potential).
 FT VARSPLIC 125 214 Missing (in isoform 4).
 FT VARSPLIC 140 185 Missing (in isoform 5).
 FT TGAAL -> TGMRGNGPCLSHWGTLGTAYGLRSQGP.
 FT LQKNLPRLSQQP (in isoform 5).
 FT /FTid=VSP_002562.
 FT Missing (in isoform 5).
 FT /FTid=VSP_002563.
 FT Missing (in isoform 3).
 FT /FTid=VSP_002564.
 FT Missing (in isoform 2).
 FT /FTid=VSP_002565.
 FT Y->F: Abolishes binding to PTPN6.
 FT S -> P (in Ref. 4).
 FT G -> R (in Ref. 4).
 FT V -> A (in Ref. 1).
 FT P -> S (in Ref. 3).
 FT L -> P (in Ref. 4).
 FT R -> K (in Ref. 3).
 FT P -> S (in Ref. 3).
 FT SEQUENCE 697 AA; 76619 MW; 6CB231CE49411D18 CRC64;
 SQ
 Query Match 95.2%; Score 2576.5; DB 1; Length 697;
 Best Local Similarity 73.0%; Pred. No. 3.9e-167;
 Matches 509; Conservative 1; Mismatches 2; Indels 185; Gaps 2;
 QY 1 MLLPLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSPYPRQDTGTPAYGYW 60
 DB 1 MLLPLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSPYPRQDTGTPAYGYW 60
 QY 61 FKAVTETTKGAPVATNQHOSREVENSTGRFQLTGDPKAGNCSLVIRDAQWQDSQHFVRV 120
 DB 61 FKAVTETTKGAPVATNQHOSREVENSTGRFQLTGDPKAGNCSLVIRDAQWQDSQHFVRV 120
 QY 121 ERGSYVRVYFMNDGFFLKVLTALTKPDVYIPETLEPQPVTVICVFNWAFEECPPPFSW 180
 DB 121 ERGSYVRVYFMNDGFFLKVLTALTKPDVYIPETLEPQPVTVICVFNWAFEECPPPFSW 180
 QY 191 TGAALSSQGYPTTSHSFVLSFTPRPDQDHTDLTCHVDFSRKGVSAQRTVLRVAYAPRD 240

Db 181 TGAALSSQGTPTTSHFVLSFTPRQDHTDNLCHVDTSKGVSVQRTVRLRAYAYAPD 240
QY 241 LVISISRDNTPD----- 252
Db 241 LVISISRDNTPALEPOFGQNVPLYEAQKQGFLLCAADSQPPATLSWVLQNRVLSSSH 300
QY 253 ----- 270
Db 301 WGPRLGLELPGVKAGDSGRYTCAENRLGSGQRAALDLSVQYPPENLRVMVSOANRTVLE 360
QY 271 NLNGTSLPVLGQSLCLVCTHSSPPARLSWTORGQVLSPPSQSPGVLLEPRVQVEHE 330
Db 361 NLNGTSLPVLGQSLCLVCTHSSPPARLSWTORGQVLSPPSQSPGVLLEPRVQVEHE 420
QY 331 GEFTCHARHPLGSGHVSLSVHY----- 354
Db 421 GEFTCHARHPLGSGHVSLSVHYSPKLLGPSCSWEAGHLHCSCSQASPAPSLRWLGE 480
QY 355 -----K 355
Db 481 ELLEGNSQDSFEVTPSSAGFWANSSLSLHGGLSGRLRCEAWNVHGAQSGSILQLPDK 540
QY 356 KGLISTAFNSGAFGLIGITALLFLCLALITMKILPKRTQTETPRPRFSRHSTILDYINV 415
Db 541 KGLISTAFNSGAFGLIGITALLFLCLALITMKILPKRTQTETPRPRFSRHSTILDYINV 600
QY 416 VPTAGPLAQKRNKATPNSPRTPLPGAPSPESKQKQYQLPSPPEPKSSTQAPESOE 475
Db 601 VPTAGPLAQKRNKATPNSPRTPLPGAPSPESKQKQYQLPSPPEPKSSTQAPESOE 660
QY 476 SQBELHYATLNFPGVPRPEARMKGTQADYAEVKFQ 512
Db 661 SQBELHYATLNFPGVPRPEARMKGTQADYAEVKFQ 697

RESULT 2

Q6UX18 PRELIMINARY; PRT; 544 AA.
AC Q6UX18;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE SIGLESC10.
GN O6FNames:UNQ477;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22857296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vasts A.,
RA Vanden R., Watanabe C., Wied D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL: AY358337; AAQ88703.1; -;
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003598; IG.c2.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; ig; 2.
DR SMART: SM00409; IG; 3.
DR SMART: SM00408; IGC2; 2.

DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 544 AA; 60267 MW; 4D84B1EF6D60AC8CB CRC64;
Query Match 83.7%; Score 2265; DB 2; Length 544;
Best Local Similarity 74.8%; Pred. No. 4.8e-146;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;
QY 1 MLLPLLSSLLGSGQAMDRFWIRVOESVMVPEGICISVPCSPSYPRODWTGSTPAYGYW 60
Db 1 MLLPLLSSLLGSGQAMDRFWIRVOESVMVPEGICISVPCSPSYPRODWTGSTPAYGYW 60
QY 61 FKAVTETTKGAPVATNHQSRREVMSRGRFOLTDGPAKGNCSLVIRDAQMDQESQYFFRV 120
Db 61 FKAVTETTKGAPVATNHQSRREVMSRGRFOLTDGPAKGNCSLVIRDAQMDQESQYFFRV 120
QY 121 ERGSVVRNFMNDGFFLVKVTALTQKPDVYIETLEPGQPVTVICVFNWAFEECPPPSPW 180
Db 121 ERGSVTVTNFMNDGFFLVKVT----- 140
QY 181 TGAALSSQGTPTTSHFVLSFTPRPQDHTDNLCHVDTSKGVSAQRTVRLRAYAYAPD 240
Db 141 -----VLSFTPRPQDHTDNLCHVDTSKGVSAQRTVRLRAYAYAPD 182
QY 241 LVISISRDNTPD----- 252
Db 183 LVISISRDNTPALEPOFGQNVPLYEAQKQGFLLCAADSQPPATLSWVLQNRVLSSSH 242
QY 253 -----PPENLRVMVSOANRTVLE 270
Db 243 WGPRLGLELPGVKAGDSGRYTCAENRLGSGQRAALDLSVQYPPENLRVMVSOANRTVLE 302
QY 271 NLNGTSLPVLGQSLCLVCTHSSPPARLSWTORGQVLSPPSQSPDGVLELPRVQVEHE 330
Db 303 NLNGTSLPVLGQSLCLVCTHSSPPARLSWTORGQVLSPPSQSPDGVLELPRVQVEHE 362
QY 331 GEFTCHARHPLGSGHVSLSVHYKKGILISTAFNSGAFGLIGITALLFLCLALITMKILP 390
Db 363 GEFTCHARHPLGSGHVSLSVHYKKGILISTAFNSGAFGLIGITALLFLCLALITMKILP 422
QY 391 KRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNKATPNSPRTPLPGAPSPESKK 450
Db 423 KRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNKATPNSPRTPLPGAPSPESKK 482
QY 451 NQKQYQLPSPPEPKSSTQAPESQBELHYATLNFPGVPRPEARMKGTQADYAEVK 510
Db 483 NQKQYQLPSPPEPKSSTQAPESQBELHYATLNFPGVPRPEARMKGTQADYAEVK 542
QY 511 FQ 512
Db 543 FQ 544

RESULT 3

AAQ88703 PRELIMINARY; PRT; 544 AA.
ID AAQ88703;
AC AAQ88703;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE SIGLESC10.
GN UNQ477.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
 Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 Godowski P.;
 "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
 Bioinformatics Assessment";
 Genome Res. 13:2265-2270(2003).
 DB EMBL: AY358337; AAC88703.1; -
 SO SEQUENCE 544 AA; 60267 MW; 4DA4E1EFD60AC8CB CRC64;
 Query Match 83.7%; Score 2265; DB 2; Length 544;
 Best Local Similarity 74.8%; Pred. No. 4.8e-146;
 Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;
 1 MLPLLLSSLLGGSOAMDGRFWRVQBSVWVPEGLCLISVPCSFSPYRQDWTGSTPAYGW 60
 1 MLPLLLSSLLGGSOAMDGRFWRVQBSVWVPEGLCLISVPCSFSPYRQDWTGSTPAYGW 60
 61 FKAVTTETKAPVATNHQREVMSTGRFQLTGDPKAGNCSLVIRDAQMDESOYFFRV 120
 61 FKAVTTETKAPVATNHQREVMSTGRFQLTGDPKAGNCSLVIRDAQMDESOYFFRV 120
 121 ERGSYRYNFMNDGFLKVTALTQKPDVYIPETLEPCQPTVICVFNWAFECPPPSFW 180
 121 ERGSYRYNFMNDGFLKVTALTQKPDVYIPETLEPCQPTVICVFNWAFECPPPSFW 180
 181 TGAALSSQGTGKPTTSHFSVLSFTPRQDHTDLTCHVDFSRKGVSAQRTVLRVAVAPRD 240
 181 TGAALSSQGTGKPTTSHFSVLSFTPRQDHTDLTCHVDFSRKGVSAQRTVLRVAVAPRD 240
 183 LVISIRDNTPALEPQPGQNVPLYEAKQGFRLRLCAADSPATLSWLVQNRVLSSSH 242
 183 LVISIRDNTPALEPQPGQNVPLYEAKQGFRLRLCAADSPATLSWLVQNRVLSSSH 242
 253 WGRPLGLELPVKGAGSGRYTCAENRLOSQQRALDLSVOYYPENLRVWVSOANRTVLE 270
 253 WGRPLGLELPVKGAGSGRYTCAENRLOSQQRALDLSVOYYPENLRVWVSOANRTVLE 270
 271 NLNGTSLPVLGOSLCLVCVTHSSPPARLSWTQGVLSPPSPDGVLELPRVQVEH 330
 271 NLNGTSLPVLGOSLCLVCVTHSSPPARLSWTQGVLSPPSPDGVLELPRVQVEH 330
 303 NLNGTSLPVLGOSLCLVCVTHSSPPARLSWTQGVLSPPSPDGVLELPRVQVEH 362
 303 NLNGTSLPVLGOSLCLVCVTHSSPPARLSWTQGVLSPPSPDGVLELPRVQVEH 362
 331 GEFTCHARHPLGSHVLSLSVHYKGLISTAFSNGAFIGITALLFLCLALIIMKILP 390
 331 GEFTCHARHPLGSHVLSLSVHYKGLISTAFSNGAFIGITALLFLCLALIIMKILP 390
 363 GEFTCHARHPLGSHVLSLSVHYKGLISTAFSNGAFIGITALLFLCLALIIMKILP 422
 363 GEFTCHARHPLGSHVLSLSVHYKGLISTAFSNGAFIGITALLFLCLALIIMKILP 422
 391 KRRTQTETPRFRSHSTILDYINVVPTAGLACKNOKATPNSPRTPPLPGAPSPESK 450
 391 KRRTQTETPRFRSHSTILDYINVVPTAGLACKNOKATPNSPRTPPLPGAPSPESK 450
 423 KRRTQTETPRFRSHSTILDYINVVPTAGLACKNOKATPNSPRTPPLPGAPSPESK 482
 423 KRRTQTETPRFRSHSTILDYINVVPTAGLACKNOKATPNSPRTPPLPGAPSPESK 482
 451 NQKQYQLPSPFPKSTQAPESQSEELHYATLNPFGVPRPEARMPKGTQADYAEVK 510
 451 NQKQYQLPSPFPKSTQAPESQSEELHYATLNPFGVPRPEARMPKGTQADYAEVK 510
 483 NQKQYQLPSPFPKSTQAPESQSEELHYATLNPFGVPRPEARMPKGTQADYAEVK 542
 511 FQ 512
 543 FQ 544

RESULT 4

BAC85493
 ID BAC85493 PRELIMINARY; PRT; 425 AA.
 AC BAC85493;
 DT 02-MAR-2004 (TRENBERL 27, Created)
 DT 02-MAR-2004 (TRENBERL 27, Last sequence update)
 DE CDNA FLJ16033 fis, clone SPLEN2001599, weakly similar to Homo sapiens
 DE sialic acid binding immunoglobulin-like lectin 8 long splice variant
 DE (Siglec8) gene.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primata; Catarrhini; Homnidae; Homo.
 NCBI TaxID=9606;
 [1]
 SEQUENCE FROM N.A.
 RP TISSUE=Splice;
 RC Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
 RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
 RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
 RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 RA Wagatsuma M., Murakawa K., Kurehori K., Takahashi-Fujii A., Oshima A.,
 RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
 RA Masuho Y., Nagai K., Isogai T.;
 RA "NEBO human cDNA sequencing project";
 RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AK122619; BAC85493.1; -
 DR EMBL;
 KW Lectin.
 SQ SEQUENCE 425 AA; 47345 MW; 809854127B397D73 CRC64;
 Query Match 80.7%; Score 2185; DB 2; Length 425;
 Best Local Similarity 87.2%; Pred. No. 1e-140;
 Matches 421; Conservative 2; Mismatches 2; Indels 58; Gaps 1;
 30 MVPEGLCLISVPCSFSPYRQDWTGSTPAYGWFKAVTTETKAPVATNHQREVMSTGR 89
 1 MVPEGLCLISVPCSFSPYRQDWTGSTPAYGWFKAVTTETKAPVATNHQREVMSTGR 60
 90 FQLTGDPKAGNCSLVIRDAQMDESOYFFRVGRSVYRYNFMNDGFLKVTALTQKPDVY 149
 61 FQLTGDPKAGNCSLVIRDAQMDESOYFFRVGRSVYRYNFMNDGFLKVTALTQKPDVY 111
 150 IPETLEPCQPTVICVFNWAFECPPPSFWTGAALSSQGTGKPTTSHFSVLSFTPRQDH 209
 112 -----VLSFTPRQDH 122
 210 DTLTCHVDFSRKGVSAQRTVLRVAVAPRDVLISIRDNTPDPPENLRVWVSOANRTV 269
 123 NDTLTCHVDFSRKGVSAQRTVLRVAVAPRDVLISIRDNTPDPPENLRVWVSOANRTV 182
 270 ENLNGTSLPVLGOSLCLVCVTHSSPPARLSWTQGVLSPPSPDGVLELPRVQVEH 329
 183 ENLNGTSLPVLGOSLCLVCVTHSSPPARLSWTQGVLSPPSPDGVLELPRVQVEH 242
 330 EGFTCHARHPLGSHVLSLSVHYKGLISTAFSNGAFIGITALLFLCLALIIMKIL 389
 243 EGFTCHARHPLGSHVLSLSVHYKGLISTAFSNGAFIGITALLFLCLALIIMKIL 302
 390 KRRTQTETPRFRSHSTILDYINVVPTAGLACKNOKATPNSPRTPPLPGAPSPESK 449
 303 KRRTQTETPRFRSHSTILDYINVVPTAGLACKNOKATPNSPRTPPLPGAPSPESK 362
 450 NQKQYQLPSPFPKSTQAPESQSEELHYATLNPFGVPRPEARMPKGTQADYAEVK 509
 363 NQKQYQLPSPFPKSTQAPESQSEELHYATLNPFGVPRPEARMPKGTQADYAEVK 422
 510 FQ 512
 423 KQF 425

RESULT 5

ID SILB HUMAN STANDARD; PRT; 686 AA.
 AC Q96RL6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Sialic acid binding Ig-like lectin 11 precursor (Siglec-11) (Sialic
 DE acid-binding lectin 11) (UNQ9222/PRO28718).
 GN Name=SIGLEC11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION WITH PTPN6 AND PTPN11.
MEDLINE=22086217; PubMed=11986327; DOI=10.1074/jbc.M202833200;
Angata T., Kerr S.C., Graves D.R., Varki N.M., Crocker P.R.,
Varki A.;
"Cloning and characterization of human Siglec-11. A recently evolved
signaling that can interact with SHP-1 and SHP-2 and is expressed by
tissue macrophages, including brain microglia.";
J. Biol. Chem. 277:24466-24474(2002).
[2]
SEQUENCE FROM N.A. (ISOFORM 2)
MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
Clark H.F., Gurney A.B., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,
Vanden K., Watanabe C., Wiscand D., Woods K., Xie M.-H., Yaneura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P., Gray A.;
"The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment.";
Genome Res. 13:2285-2270(2003).
CC -1- FUNCTION: Putative adhesion molecule that mediates sialic-acid
dependent binding to cells. Preferentially binds to alpha2,8-
linked sialic acid. The sialic acid recognition site may be masked
by cis interactions with sialic acids on the same cell surface. In
the immune response, may act as an inhibitory receptor upon ligand
induced tyrosine phosphorylation by recruiting cytoplasmic
phosphatase(s) via their SH2 domain(s) that block signal
transduction through dephosphorylation of signaling molecules.
CC -1- SUBUNIT: Interacts with PTPN6/SHP-1 and PTPN11/SHP-2 upon
phosphorylation.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q96RL6-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q96RL6-2; Sequence=VSP_008764;
CC -1- TISSUE SPECIFICITY: Expressed by macrophages in various tissues
including Kupffer cells. Also found in brain microglia.
CC -1- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to
as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This
motif is involved in modulation of cellular responses. The
phosphorylated ITIM motif can bind the SH2 domain of several SH2-
containing phosphatases.
CC -1- PTM: Phosphorylated on tyrosine residues.
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
(sialic acid binding Ig-like lectin) family.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement. Usage by and for commercial
or send an email to license@sib-sib.ch.
CC -----
CC EMBL: AF337818; AAK72907.1; -
CC EMBL: AV358135; AAK88502.1; -
CC HSSP: Q9Y286; I078.
CC Genew: HGNC:15622; SIGLEC11.
CC MIM: 607157; -
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003006; Ig_MHC.
CC Pfam: PF00047; ig_3.
CC PROSITE: PS50835; IG_LIKE; 3.

DR PROSITE; PS00290; IG_MHC; 1.
KW Alternative splicing; Cell adhesion; Glycoprotein;
KW Immunoglobulin domain; Lectin; Phosphorylation; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 15 Potential.
FT CHAIN 16 686 Sialic acid binding Ig-like lectin 11.
FT DOMAIN 16 549 Extracellular (Potential).
FT TRANSMEM 570 572 Potential.
FT DOMAIN 573 686 Cytoplasmic (Potential).
FT DOMAIN 19 122 Ig-like V-type.
FT DOMAIN 147 232 Ig-like C2-type 1.
FT DOMAIN 239 338 Ig-like C2-type 2.
FT DOMAIN 343 440 Ig-like C2-type 3.
FT SITE 630 635 ITIM motif.
FT DISULFID 37 174 By similarity.
FT DISULFID 42 102 By similarity.
FT DISULFID 165 216 By similarity.
FT DISULFID 275 322 By similarity.
FT DISULFID 379 424 By similarity.
FT CARBOHYD 43 43 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 78 78 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 250 250 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 354 354 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 363 363 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 485 485 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 503 503 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 443 539 YPQLLGSCWEAEGLHSCSSQASAPSLRWMLGEELLE
GNSSQGSFEVTPSSAGPWANSSLSLHGSLSGSLRCKAWN
VHQAQSGSVFOLLPG -> W (in isoform 2).
/FTid=VSP_008764.
FT CONFLICT 84 84 E -> A (in Ref. 2).
FT CONFLICT 353 353 A -> G (in Ref. 2).
FT SEQUENCE 686 AA; 74544 MW; FDOEAL1936158E5A8 CRC64;
Query Match 55.9%; Score 1513.5; DB 1; Length 686;
Best Local Similarity 46.6%; Pred. No. 1.1e-94;
Matches 323; Conservative 51; Mismatches 102; Indels 217; Gaps 6;
QY 1 MLLPILLSSLLGSGQANDGRFWIRVOESVMYVPEGLICISVPCSFYPRQDWTGSTPAICYW 60
DB 2 LLLPILLPVLGAGSLNKDPSYSLQVQRPVPEGLCVIVSCNLSYPRDGDWDETAAYGYW 61
QY 61 FKAVTETTKGAPVATNHSQREVENSTGRFOLTGDPKAGNCSLVIRDAQMDQESQYFPRV 120
DB 62 PKGRTSPKTGAPVATNHSQREVENSTGRFOLTGDPKAGNCSLVIRDAQREDAWYFPRV 121
QY 121 ERGSVVRNFMNDGFFLKVTALTOKPDVYIPETLEPGQPVTVICVFNWAPBECPPPSFSW 180
DB 122 ERGSVRHSFLSNAFFLKVTALTOKPDVYIPETLEPGQPVTVICVFNWAPKCPAPFSW 181
QY 181 TGAALSSOGTKPTTSHFSVLSTPRPODHTDLTCHVDFFSRKGYSAQRTVLRVAYAPRD 240
DB 182 TGAALSPRTPTSHFSVLSTFTSPQDHDLDLCHVDFFSRKGYSAQRTVLRVAYAPKD 241
QY 241 LVISISRDNTPD----- 252
DB 242 LIISISHDNTSALELQGNVILEYVQKQFLRLCAADSQPPATLSWVLQDVLSSSHPWG 301
QY 253 -----PPENLRVWVSOANETVLENL 272
DB 302 PRTGLELRVAGDSGRYTCRAENRLGSSQQAALDLVSQVPPENLRVWVSOANETVLENL 361
QY 273 GNGTSLPVLQGSCLVLCVTHSSPPARLSWTQGVLSPSQSPDGVLELPRVQVEHEGE 332
DB 362 GNGTSLPVLQGSCLVLCVTHSSPPARLSWTQGVLSPSQSPDGVLELPRVQVEHEGE 421
QY 333 FTCHARHPLGSHVLSLSVHYKGLSTAFS----- 364
DB 422 FTCHAQHPGLGSHVLSLSVHYKGLSTAFS----- 481
QY 365 ----- 364
DB 482 LEGNSSQGSFEVTPSSAGPWANSSLSLHGSLSGSLRCKAWN VHGAGSGSVFOLLPGK 541


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RN RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861;
RA Shiba H., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishize T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA "AIKEN integrated sequence analysis (KISA) system-384-Format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
[6]
RN RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kuribara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saichoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK042488; BAC31272.1;
DR HSSP: Q9Y286; 1078.
DR MGD: MGI:2443630; Siglec10.
DR GO: GO:0005529; F:sugar binding; IEA.
DR GO: GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003598; Ig_c2.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00408; IGG2; 2.
DR PROSITE: PS00835; IG_LIKE; 3.
KW Lectin.
FT NON_TER
SQ SEQUENCE 623 623 69384 MW; 5827C09D52C3AC7F CRC64;

Query Match 44.8%; Score 1211.5; DB 2; Length 623;
Best Local Similarity 43.8%; Pred. No. 3.7e-74;
Matches 267; Conservative 55; Mismatches 111; Indels 187; Gaps 8;

QY 2 LLELLSSLLGSGQANDGRFWRVQSVVMVPEGLCISVPCFSYPRQDWTGSTPAYGYWF 61
Db 3 LLLFLLSFLLDGPGQGMESYFLQVQIRVKAQEGLCIFVPCFSYSPGKWLNSPLYGYWF 62
QY 62 KATETTKAPVATNQSREVENSTGRFQLTCDPAKGNCSLVIRDAQMDSQYFFRVE 121
Db 63 KGRKPSLGFPPVATNNKDKVLEWAEAGRFQLLDISKNCSLIKDVQGDSTNYFFRVE 122
QY 122 RGSYRVNFMNDGFFLVKTALTKQPVYIPETLEPGQPVTVICVFNWAEFCPPPSFSMT 181
Db 123 RG-FERFSPEE-FRLOVEALTKQPIFIPVLEPGEPVTVVCLFSWTNQCPSPSWM 180
QY 182 GAALSSCGTKPTTSHSVLSFTPRPODHDITLCHVDPSRKGVSAGRTVRLRVAYAPRDL 241
Db 181 GDAVSQESRPHTSNYSVLSFIPGLQHDITELTCLQDFSR--MSTORTVRLRVAYAPRSL 238
QY 242 VISISDGN--TPD----- 252
Db 239 AISIFHDNVSVDLHENPSHLEVVQCGQSURLLCTADSQPPALSLWLEQVLSWSVGS 298
QY 253 -----PPENLRVMSQANRTVLENLG 273
Db 299 RTLALPELPMWKAGDSGHYTCQAEENRLGSOQHTLDLSVLPQDRLRVTSQANRTVLEILR 358
QY 274 NGTSLPVLGOSLCLVCTVTHSSPRLSWTQRCQVLSPSQSPDPGLVLELPRVQVEHGEF 333
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Db 359 NAISLPVLGOSLCLVCTVSNPPANVSWAVVTQTLPIQSSEPGVLELPLVQREHEGEF 418
QY 334 TCHARHPGLGSOHVSLSLVHY-----KKGLE----- 358
Db 419 TCAQNPLGAORISLSLSVHYPPQWSSPSCSWKAGLHCNCSSRAWPAPSLRWLREGGL 478
QY 359 -----IS 360
Db 479 EGNSSNASFTVFFSGLGPGWVNSLSLQELGSPSLWLSCESNWTHGAQTTSVLLLPDKDSA 538
QY 361 TAFNSGAFGLGITALLFLCLALILMKLPKRTQETPRPRFSRHSHTILDYINVVPTAG 420
Db 539 TAFSGAVLGFGITALLALCLIVIVTKLQKKGQEBSPRPKJRGSGTILDIYINVVPR 598
QY 421 PLAQRNOKATPNSPRTPPLP 440
Db 599 SLA--RNWKAEPDAPSRSSP 616

RESULT 8
Q72728 PRELIMINARY; PRT; 499 AA.
ID Q72728 AC Q72728;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1] SEQUENCE FROM N.A.
RP TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raba S.S., McQuellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC053319; AAH53319.1;
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003598; Ig_c2.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00408; IGG2; 1.
DR PROSITE: PS00835; IG_LIKE; 2.
KW Hypothetical protein.
SQ SEQUENCE 499 AA; 54052 MW; CA32FEF7A88A7D3D CRC64;

Query Match 35.3%; Score 955; DB 2; Length 499;
Best Local Similarity 42.3%; Pred. No. 8.4e-57;
Matches 224; Conservative 70; Mismatches 160; Indels 76; Gaps 13;
```


(sialic acid binding Ig-like lectin) family.

-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

-!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.

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EMBL; AF277806; AAK51233.1; -
 EMBL; AF277806; AAK51234.1; -
 EMBL; AF282256; AAK71521.1; -
 EMBL; AY358140; AAK88507.1; -
 EMBL; BC015809; AAK85809.2; -
 HSP; Q9Y286; 107S.
 GenBank; HGNC:15482; SIGLECL1.
 InterPro: IPR007110; Ig-like.
 Pfam: PF00047; ig; 4.
 PROSITE; PSS0835; IG_LIKE; 3.
 Alternative splicing; Cell adhesion; Glycoprotein;
 Immunoglobulin domain; Lectin; Polymorphism; Repeat; Signal;
 Transmembrane.
 SIGNAL 1 18 Potential.
 CHAIN 19 595 Sialic acid binding Ig-like lectin-like
 DOMAIN 19 481 Extracellular (Potential).
 TRANSMEM 482 502 Potential.
 DOMAIN 503 595 Cytoplasmic (Potential).
 DOMAIN 19 142 Ig-like V-type 1.
 DOMAIN 143 269 Ig-like V-type 2.
 DOMAIN 275 358 Ig-like C2-type 1.
 DOMAIN 365 462 Ig-like C2-type 2.
 SITE 563 568 ITIM motif.
 SITE 586 591 SLAM-LIKE MOTIF.
 DISULFID 44 104 By similarity.
 DISULFID 166 299 By similarity.
 DISULFID 171 231 By similarity.
 DISULFID 293 342 By similarity.
 DISULFID 401 446 By similarity.
 CARBOHYD 140 140 N-linked (GlcNAc...) (Potential).
 CARBOHYD 179 179 N-linked (GlcNAc...) (Potential).
 CARBOHYD 230 230 N-linked (GlcNAc...) (Potential).
 CARBOHYD 290 290 N-linked (GlcNAc...) (Potential).
 CARBOHYD 360 360 N-linked (GlcNAc...) (Potential).
 CARBOHYD 367 367 N-linked (GlcNAc...) (Potential).
 CARBOHYD 385 385 N-linked (GlcNAc...) (Potential).
 VARSPLIC 4 141
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 SFSPQNGWTFADSPVHGYPFRAGDHVSRNIPVATNNPARAV
 QETDRPHLLGDPQNKDCTLSIRDTRSDAGTYVFCVBERG
 NMKNVYDOLSVNV -> PLLWANEEDSGGWADPRFS
 (in isoform Short).
 /FTID=VSP_002566
 P->T (in dBSNP:2034891).
 /FTID=VAR_014259.
 R->W (in Ref. 3).
 VARIANT 81 81
 CONFLICT 528 528
 SEQUENCE 595 AA; 64984 MW; D05662176274C5C3 CRC64;
 Query Match 33.6%; Score 909; DB 1; Length 595;
 Best Local Similarity 41.1%; Pred. No. 1.4e-53;
 Matches 211; Conservative 65; Mismatches 174; Indels 40; Gaps 10;
 7 LSELGGSQAMGRFWRVQSVNVEGLCISVPCSFSPRODWTGSTPAYWYKAVTE 66
 137 LSNVTASQDLLGRYRLEVPESVTQEGLCVSPVLYPHVYNTWASSPVYGSWFKEGAD 196
 67 TTKGAPVATNHQREVMSPTRGFQLTGDPKNCSLVIRDAQMDQESQYFFRVERGSV 126
 197 IPWDIPVATNPSGKQVQETHGFLLLGDPQTNCSLIRDAKSGDKYKQVERGSR- 255

QY 127 RYNEWMDGFFLKVTALQKPDVIVPETLEPGOPVTVICVFNWAFEECPPPSFWGTGAALS 186
 DB 256 KWNYYDKLSVHVHTALHTMTFTSPGLESGHERNLTCVPMACEQGTPTTIWMGASVS 315
 QY 187 SQGKPTTSHFSVLSTPFRQDHDITDCTHVDFSRKQVSAQRTVRLVAVAPRDLVISIS 246
 DB 316 S-LDPTITRSSMLSLIPQPDHGTSLTQVTLPGAGVTMTAVRLNISV----- 363
 QY 247 RNTFDPENLRVMSQANRTVLENLGNSTLPVLEGSCLVGVTHSSPPARLSWTORG 306
 DB 364 -----PQNUTMTVFOGDGTASTLRNGSALSVLGQSLHLVCAVDNSNPAPRLSWTWS 417
 QY 307 QVLSFQSPDGVLEPRVQVEHEGEFTCHARHPLGSHQVLSLSVHYK---KGLISTAF 363
 DB 418 LTLSPSQSSNLGVLEPRVHVWDEGEFTCAQNLGSHQVLSLSLQNEVTGKMRPISGV 477
 QY 364 SNGAFLGIGITALLFLCLALIMKILPKRTQTETPRPRSRHSTILDYINVV---PTAG 420
 DB 478 TLGAFGGAGATLAVFLVFCIFVVV---RSCRKKSARPAVGVGTGMDANAVGASQSG 534
 QY 421 PLACKRNQKATPNSPRTPLPP--CAPSPESKXNKQVQLPSPFEPKSKSTQAPESQESQE 478
 DB 535 PLI-----ESPADDSPPHAPALATPSPE-----EGEIQVASLSFHKARQYPOQEA-I 584
 QY 479 ELHYATLNFP 488
 DB 585 GYEYSEINIP 594
 RESULT 11
 SILL_PANTR
 ID SILL_PANTR STANDARD; PRT; 597 AA.
 AC Q95LH0;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Sialic acid binding Ig-like lectin-like 1 precursor (Siglec-like molecule 1) (Siglec-L1).
 GN Name=SIGLECL1;
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_taxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21523976; PubMed=11546777; DOI=10.1074/jbc.M105926200;
 RX Angata T., Varki N.M., Varki A.;
 RT "A second uniquely human mutation affecting sialic acid biology.";
 RL J. Biol. Chem. 276:40282-40287(2001).
 CC -!- FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell surface.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in modulation of cellular responses. The phosphorylated ITIM motif can bind the SH2 domain of several SH2-containing phosphatases.
 CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (sialic acid binding Ig-like lectin) family.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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EMBL; AF293372; AA109302.1; -